

STIC-Biotech/ChemLib

131534

From: Hutzell, Paula
Sent: Wednesday, September 01, 2004 3:39 PM
To: Graser, Jennifer; STIC-Biotech/ChemLib
Subject: RE: rush search

approved

-----Original Message-----

From: Graser, Jennifer
Sent: Wednesday, September 01, 2004 3:13 PM
To: Hutzell, Paula
Subject: rush search
Importance: High

Hi Paula,
Could you please authorize this rush search for an Election?
Thanks, Jennifer

STIC:

Please search jnucleotides 918-1580 of SEQ ID NO: 12 from 10/625,221 in
pending and commercial databases.

Thanks,
Jennifer Graser
REM 3B09 (mailbox 3C18)
Art Unit 1645
272-0858

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 3, 2004, 17:15:56 ; Search time 2409 Seconds
(without alignments)
8218.608 Million cell updates/sec

Title: US-10-625-221-12_COPY_918_1580

Perfect score: 663

Sequence: 1 caacaagaccgacgaag.....aagttacctaacaacaaag 663

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_estum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hci:*

9: gb_est1:*

10: gb_est2:*

11: gb_hci:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vri:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78.8	11.9	1101	29	CNS00EVL
C 2	77.4	11.7	1101	29	CNS0039G
C 3	72.8	11.0	994	13	AX414650
C 4	72.4	10.9	1201	29	CNS0167M

C 5	71.4	10.8	821	29	CNS0090X
C 6	69.6	10.5	1101	29	CNS001FB
C 7	69.4	10.5	1201	9	AL565455
C 8	68.6	10.3	1056	13	AX415058
C 9	68	10.3	1201	9	AL536104
C 10	67.6	10.2	840	29	CNS06V50
C 11	67.6	10.2	1201	9	AL536104
C 12	66.6	10.0	1201	13	AX439779
C 13	66	10.0	1200	13	AX437739
C 14	65.8	9.9	945	29	CNS04DOK
C 15	65.8	9.9	1101	29	CNS0039G
C 16	65.6	9.9	999	13	AX380865
C 17	65.2	9.8	1201	13	AX364179
C 18	65	9.8	1200	13	AX436510
C 19	64.8	9.8	853	29	CG767791
C 20	64.4	9.7	759	29	CNS06QXV
C 21	64.4	9.7	1201	9	AL531981
C 22	64.2	9.7	1043	29	CNS0145P
C 23	64	9.7	1200	13	AX415878
C 24	63.6	9.6	1199	13	AX375702
C 25	63.4	9.6	1101	29	CNS008X3
C 26	63.4	9.6	1126	13	AX446388
C 27	63.4	9.6	1200	13	AX415878
C 28	63.2	9.5	1008	14	CD329035
C 29	63.2	9.5	1201	13	AX462660
C 30	63.2	9.5	1896	29	CG753083
C 31	63	9.5	1200	29	CNS016CO
C 32	62.8	9.5	996	29	CNS00FUH
C 33	62.6	9.4	886	28	BH177277
C 34	62.6	9.4	886	29	CNS07JUX
C 35	62.6	9.4	1101	29	CNS0039L
C 36	62.6	9.4	1318	29	CG752908
C 37	62.4	9.4	1201	9	AL532464
C 38	62.2	9.4	1165	13	AX338369
C 39	62.2	9.4	1200	13	AX437758
C 40	62	9.4	986	13	AX366417
C 41	62	9.4	1064	13	AX361825
C 42	62	9.4	1101	29	CNS017V2
C 43	62	9.4	1169	29	CNS06RHQ
C 44	61.8	9.3	932	9	AL514901
C 45	61.8	9.3	1001	29	CNS0155H

ALIGNMENTS

RESULT 1

CNS00EVL

LOCUS

DEFINITION

BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CNS00EVL 1101 bp DNA linear GSS 04-JUN-1999

Drosophila melanogaster genome survey sequence T7 end of BAC:

BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL069706

AL069706.1 GI:4949849

GSS.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers

1..1101

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone="BACR29B23"

/clone_lib="RPCI-98"

/note="end: 17"

ORIGIN

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Query Match      11.9%; Score 78.8; DB 29; Length 1101;
Best Local Similarity 31.8%; Pred. No. 3.1e-05;
Matches 193; Conservative 109; Mismatches 305; Indels 0; Gaps 0;

QY 10 CCGATCCAGCACTTCACAGATCTAGTTAGTTAAACCTTCAAAATATATATTT 69
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
395 CCCCSCGMMMSCCACACCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 454
QY 70 CTTTATGAGGGTGACCTGTTACTCAGAGATGCGAATCTGTTGATCAACTTTATCT 129
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
455 TCTCAHTTMMOMMMWAAATWTWAAWAAWTTTAAATWAAWAAWAAWAAWAAWAAW 514
QY 130 CACCATTAAATATAATGTTTCAGGGCCAAATTTATGAATTTAAATGAACTTAAG 189
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
515 WWTWATTTTAAWTTAAWTTAAWTTAAWTTAAWTTAAWTTAAWTTAAWTTAAWTT 574
QY 190 AACCAAGAGATGCGCACTTTATTAAGGATAAAACGTTGAPATTTATGTTGATCAAT 249
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
575 AWAATWATATTAATWATATAATWATATAATWATATAATWATATAATWATATAATW 634
QY 250 TACCATCTCTGTTATTTATGCAAAATGCAGAAAGGAGTGCATGTATCTACGAGGGGTA 309
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
635 TAATAATTTAATWTTAATAATWTTAATAATWTTAATAATWTTAATAATWTTAATAA 694
QY 310 ACAATATCATGAGGGAATCATTTAGAAATTCCTAAAAAGATAGTGTAAAGTCAATC 369
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
695 AAAAAAATAAATAWAAWATWATAWATAWATAWATAWATAWATAWATAWATAWATAW 754
QY 370 GATGATCCAAAGCCTATCATTTGATATTGAACAAATAAAAAATGTTACTGCTCAA 429
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
755 TATWATATATATWTTTAAWTTAAWTTAAWTTAAWTTAAWTTAAWTTAAWTTAAW 814
QY 430 GAATTAGACTATAAAGTTAGAAATATCTTACAGATAATAAGCAACTATATCTAATGGA 489
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
815 AATWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAW 874
QY 490 CTTCTAAATATGAACCTGGATATATAAGTTTCATACCTAAGAAATAAAGAAAGTTTGG 549
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
875 AAAAAATAWTTTWTWTTTAAWTTAAWTTAAWTTAAWTTAAWTTAAWTTAAWTTAA 934
QY 550 TTTGATTTTCCCTGACCAAGCAATTTACTCAATCAATATCTTATGATATATAAAGAT 609
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
935 AWWTTWATATTTTAAATWTTAAWTTAAWTTAAWTTAAWTTAAWTTAAWTTAAWTT 994
QY 610 AATGAAA 616
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
995 WWTWATA 1001

```

RESULT 2

CNS0039G/c

LOCUS

DEFINITION

CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

AL063921

AL063921.1 GI:4941778

VERSION

GSS.

KEYWORDS

Drosophila melanogaster (fruit fly)

SOURCE

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

ORGANISM

1 (bases 1 to 1101)

REFERENCE

Genoscope.

AUTHORS

Direct Submission

TITLE

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr)

- Web : www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mamoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain Y2; cn bw sp, the same strain used for the BDGP's

P1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers

1..1101

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone="BACR08K10"

/clone_lib="RPCI-98"

/note="end: TET3"

ORIGIN

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Query Match      11.7%; Score 77.4; DB 29; Length 1101;
Best Local Similarity 20.0%; Pred. No. 5.6e-05;
Matches 112; Conservative 230; Mismatches 215; Indels 2; Gaps 1;

QY 38 GTTTAGTTAAAAACCTTCAAAATATATATTTTCTTATGAGGTGACCTGTACTCAG 97
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
956 GKXKKAAXAAWATWATWATWATWATWATWATWATWATWATWATWATWATWATW 897
QY 98 AGAATGTGAAATCTGTTGATCAACTTTTATCTCAACATTTAATATATATATGTT 157
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
896 TKDDDDKDKWDDWAKGTWGDATWAAATDWWMGWADADWTTWDAADDDWADWDWA 837
QY 158 CAATATGATATAATTAATAAACTGNACTTAAGAACCAAGATGCAACTTTATTAGG 217
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
836 WAKWDDAWAGARTADRRDWDGDRAGKRGKRRDRKRRDRKDDKDDAADDRAATTT 777
QY 218 ATAAAAAGCTTGATATTTATGTTAGAAATATTACCATCTCTGTTATTATGTAAG 277
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
776 TTTTRDTHDWWKKTUWTRWADRTWDRDTRDTRDTRDTRDTRDTRDTRDTRDTR 717
QY 278 CAGAAAGGATGATGATATCTACGAGGGGTAAACAAATCATGAAGGGGAATCATTTAG 337
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
716 DADADDTRDRRRRRGGDAGAGKGTGRKRRRRDRATWDRDTRDTRDTRDTRDTRD 657
QY 338 TTCCTAAAAAGATAGTCGTTTAAAGTATCAATCGATGGTATCCAAAGCCTATCAT 397
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
656 DDWDRDRRRKRRRRRTTAAAWDWWTWKAWDWKTRDRDRDRDRDRDRDRDRDR 597
QY 398 TTGAAACAAATAAAAAATGCTAAGTAATAGACTATAAAGTTAGAAATATC 457
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
596 ADRWAKARAEAREDDRA--RAADRRTWTTKGTATTATTTTAAWAAWAAWAAWAT 539
QY 458 TTACAGATAATAAGCAACTATATCTAATGAGCCTTCTAAATATGAACCTGATATA 517
Db ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :

```



```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 1056)
AUTHORS    Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL    Unpublished (2001)
COMMENT    Contact: Genoscope
           Genoscope - Centre National de Sequencage
           BP 191 91006 EVRY cedex - France
           Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
           Library was constructed by Life Technologies, a division of
           Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
           http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
           Faraday Avenue Genoscope sequence ID : CS0CAP004ADL0NF1.

FEATURES             Location/Qualifiers
     source            1..1056
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0CAP004Y319"
                     /tissue_type="THYMUS"
                     /clone_lib="Homo sapiens THYMUS"
                     /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."

ORIGIN
Query Match      10.3%; Score 68.6; DB 13; Length 1056;
Best Local Similarity 35.8%; Pred. No. 0.0025;
Matches 186; Conservative 79; Mismatches 250; Indels 5; Gaps 1;

QY 128 CTCACATTTAATATATTAAGTTCAGGCCAAATATGATAAATTAATAAACTGAACCTTA 187
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 188 AGAACCAAGAGATGCAACTTTATTAAGGATAAAGCGTTGATATTTATGCTAGATAT 247
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 412 AWWTKATATATATTTTATTTATTAATAAAGAAATATATATTTTAAATAAATAAAT 471
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 248 ATTACCATCTCTGTTTATTAATG-----TCGAAATGCAGAAAGAGTGATGATCTACGG 302
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 472 TTTWAAAAAATAAATTTTATWAAATTTWAAAAAATAAATTTWKKKWTATATAAAAAA 531
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 303 AGGGTAAACAATCATGAAGGAATCATTTGAAATTCCTAAAAAGATGCTGTTAAAGT 362
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 532 AAAAAAATAAATAAATAATATATATTTATATATATAAATAAATAAATAAATAAATAA 591
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 363 ATCAATCATGATATCCAAAGCCTATCATTTGATATTCGAAACAAATAAATAAATGCTAAC 422
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 592 AAAAAAATAAATTTGAAATATGTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 651
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 423 TGCTCAAGAAATAGACTATAAGTTAGAAATATCTTACAGATATAAAGCAACTATATAC 482
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 652 TTTTWTADWDATWAATATATTTTGTGAGWAAAAAATAAATAAATAAATAAATAAATAA 711
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 483 TAATGGACCTCTAAATAGAACTGGATATATAAAGTTTCATACCTAAGAAATAAAGAAAG 542
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 712 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 771
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 543 TTTTGGTTGATTTTTTCCCTGACCAAGAAATTTTACTCAATCAATATCTTATGATATA 602
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 772 AWWWWWWTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 831
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 603 TAAAGATAATGAAGCGTTGATCTCAACACACAGCAAGCAAT 642
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 832 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 871
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

AL536104
LOCUS      AL536104      1201 bp      mRNA      linear      EST 31-MAY-2003
DEFINITION CS0DF022YC18 5-PRIME, mRNA sequence.
ACCESSION  AL536104
VERSION    AL536104.2 GI:31260974
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1 (bases 1 to 1201)
AUTHORS    Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL    Unpublished (2001)
COMMENT    On Feb 13, 2001 this sequence version replaced gi:12799597.
           Contact: Genoscope
           Genoscope - Centre National de Sequencage
           BP 191 91006 EVRY cedex - France
           Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
           Library was constructed by Life Technologies, a division of
           Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
           http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
           Faraday Avenue Genoscope sequence ID : CS0DF022B09QPI.

FEATURES             Location/Qualifiers
     source            1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DF022YC18"
                     /tissue_type="FETAL BRAIN"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."

ORIGIN
Query Match      10.3%; Score 68; DB 9; Length 1201;
Best Local Similarity 32.5%; Pred. No. 0.0031;
Matches 169; Conservative 101; Mismatches 249; Indels 1; Gaps 1;

QY 98 AGAATGCGAATCTGTCATCAACTTTTATCTCACCATTATATATATATATATATATAT 157
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 678 AAATTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 737
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 158 CAAATTTATGATAAAATTAATAAACTGAACTTAAGAACCAAGAGATGCGCACTTTATTAAGG 217
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 738 TWAATATATATTTTATATATATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 797
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 218 ATAAAAAGTTGATTTATGCTGTGAGAAATATACCATCTCTGTTATTTATGTAAGAAATG 277
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 798 WTTWKATTAATATAAATTAATTTTAAWTTTATTTTATTTATTTATTTATTTATTTATTT 857
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 278 CAGAAAGGAGTGTGATCTACGGAGGGTAAACAATCATCAAGGAGGATCATTTAGAA 337
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 858 TTTTATAAATAATTTATTTTAAATTTTAAWTTTATTTTATTTTATTTTATTTTATTTA 917
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 338 TTCCTAAAAAGATAGTGTGTTAAAGTATCAATCGATGGTATCCAAAGCCTATCATTTGATA 397
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DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 398 TTGAAAACAATAAATAAATGCTACTGCTCAAGATTTAGACTATAAAGTTAGAAATAATC 457
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 458 TTACAGATAATAAGCAACTATATATACTAATGCACTCTCTCAATATGAACCTGATATATA 517
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1038 AAAATATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1097
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 518 AGTTCATACCTAAGAAATAAGAAAGTTTTTGGTTTGTAT-TTTTTCCCTGAAACCAAGATTT 576
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 504 AACTGGATATATAAGTTTCATACCTAAGATAAAGAAAGTTT 546
Db 903 TATAAAAAAAAAAAAAAAAAATTTTAAAAAATAAATAATAT 945

RESULT 15
CNS0039G      1101 bp      DNA      linear      GSS 03-JUN-1999
LOCUS      Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION      BACR08X10 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION      AL063921
VERSION      AL063921.1 GI:4941778
KEYWORDS      GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM      Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 1101)
AUTHORS      Genoscope.
TITLE      Direct Submission
JOURNAL      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT      Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mamoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            p1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.
FEATURES             source
    1..1101
        /organism="Drosophila melanogaster"
        /mol_type="genomic DNA"
        /db_xref="taxon:7227"
        /clone="BACR08X10"
        /clone_lib="RPCI-98"
        /note="end : TET3"

ORIGIN
Query Match      9.9%; Score 65.8; DB 29; Length 1101;
Best Local Similarity 21.9%; Pred. No. 0.0083;
Matches 115; Conservative 198; Mismatches 211; Indels 1; Gaps 1;

QY 138 AATATATAATGTTTCAGGGCCAAATATGATAAATTAATAAACTGAACCTTAAGAACCAAGA 197
Db 395 MATATATAAATTTTATTAATAAATAAATAATTTTAAATAAATAAATAATTTTAAATAA 454

QY 198 GATGGCAACTTATTATTAAGGATAAAGACCTTGATATTTATGTTGTTAGATATATACCATCT 257
Db 455 AAATAATATTTTAAATAAATAAATAAATAATTTTATTTTATTTTATTTTATTTTATTTT 514

QY 258 CTGTTATTTATGTTGAATGCGAAGAGAGTGCATGATCTACGGAGGGGTAAACAATCA 317
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QY 318 TGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGCTGTTAAAGTATCATCGATCGTAT 377
Db 575 YTTTYYHYTYTYTTHYTHYTHYTHYTHYTHYTHYTHYTHYTHYTHYTHYTHYTHYTHYTH 633

QY 378 CCAAGCCATCATTTGATATGAACAAATTAATAAATAAATAAATAAATAAATAAATAAATA 437

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Db 634 TTTAAYYYTCTMYYYHYHMHHAHAHAHAHAHAHAHAHAHAHAHAHAHAHAHAHAHAHAHA 693
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Db 694 CTTTCHHCYYYHYHHTAHHHTTHHWAHYHYHYHMYHMYHMYHMYHMYHMYHMYHMYHMYHMY 753
QY 498 ATATGAAACTGGATATATAAAGTTTCATACCTAAGATAAAGAAAGTATTTTGGTTTGTATTT 557
Db 754 HTTWAVAHAMMMHHAHYAAAAAATAATTHVHHTTHYMHHTYMHHTYMHHTYMHHTYMHHTYMH 813
QY 558 TTTCCCTGAACACAGATTTTACTCAATCTAAATATCTTATGATATATAAAGATAAATAAGAAC 617
Db 814 HCWHYYHTAATCTCTWTHHEWMTTWHYHHTTHHHTTTHWAWHHTTTHWAWHHTTTHWAWHHT 873
QY 618 GCTTGACTCAACACACAGCCAAATTTGAAGTCTTACCTAACAACAA 662
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Search completed: September 3, 2004, 18:56:46
Job time : 2413 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 3, 2004, 17:19:26 ; Search time 77 Seconds
(without alignments)
4778.343 Million cell updates/sec

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Perfect score: 663
Sequence: 1 caacaagaccgacccaag.....aagtcactaacacaacaaag 663

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	661.4	99.8	1837	2	US-08-743-637B-33
3	661.4	99.8	1837	3	US-08-526-840B-33
4	658.2	99.3	1837	4	US-09-144-776B-15
5	166.8	25.2	773	1	US-08-446-918A-1
6	166.8	25.2	773	2	US-08-580-806-1
7	166.8	25.2	773	4	US-08-144-776B-5
8	164.2	24.8	1095	4	US-09-144-776B-13
9	158.8	24.0	723	4	US-09-350-755A-3
10	158.8	24.0	801	4	US-09-350-755A-2
11	158.8	24.0	1388	4	US-09-144-776B-9
12	158.8	24.0	1712	4	US-09-144-776B-7
13	112	16.9	815	4	US-09-144-276-7
14	71	10.7	757	4	US-09-144-776B-3
15	71	10.7	757	4	US-09-350-755A-1
16	71	10.7	830	4	US-09-144-776B-1
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19	59	8.9	751	1	US-08-446-918A-3
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21	52.4	7.9	640681	4	US-09-790-988-1
22	50.8	7.7	19124	2	US-08-487-826B-13
23	48.6	7.3	1664976	4	US-08-916-421B-1
24	48.4	7.3	4185	4	US-09-417-485D-7
25	48.4	7.3	10640	4	US-09-417-485D-5
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C	28	47	7.1	53332	4	US-09-801-861-3	Sequence 3, Appli
	29	46.8	7.1	1374	4	US-09-601-198-158	Sequence 158, App
	30	46.8	7.1	7218	1	US-08-232-463-14	Sequence 14, Appl
	31	46.8	7.1	10467	4	US-10-204-708-2	Sequence 2, Appli
	32	46.4	7.0	665	2	US-08-883-785A-36	Sequence 36, Appl
	33	46.4	7.0	1851	4	US-09-601-198-51	Sequence 51, Appl
	34	46.2	7.0	660	1	US-07-991-867B-32	Sequence 32, Appl
	35	46.2	7.0	660	2	US-08-107-755A-32	Sequence 32, Appl
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	41	46.2	7.0	1511	4	US-09-370-861A-8	Sequence 8, Appli
	42	46.2	7.0	4810	3	US-08-852-629-11	Sequence 11, Appl
	43	46.2	7.0	4838	3	US-08-852-629-15	Sequence 15, Appl
	44	45	6.8	5152	4	US-10-204-708-73	Sequence 73, Appl
	45	45	6.8	11015	4	US-10-204-708-55	Sequence 55, Appl

ALIGNMENTS

RESULT 1
US-08-973-391C-12
; Sequence 12, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Rosigiani, Manuela
; APPLICANT: Stoeher, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (828)..(1583)
; OTHER INFORMATION:
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661 AAG 663
Db
1578 AAG 1580

RESULT 2

US-08-743-637B-33
; Sequence 33, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:

; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.

; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

; NUMBER OF SEQUENCES: 273

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN

; COUNTRY: USA

; ZIP: 53202-4497

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/743,637B

; FILING DATE: 04-NOV-1996

; CLASSIFICATION: -435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/526,840

; FILING DATE: 11-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: BAKER, Jean C.

; REGISTRATION NUMBER: 35,433

; REFERENCE/DOCKET NUMBER: 850586.90012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (414) 277-5000

; TELEFAX: (414)277-5591

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1837 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pyogenes
US-08-743-637B-33

Query Match 99.8%; Score 661.4; DB 2; Length 1837;

Best Local Similarity 99.8%; Pred. No. 2e-143;
Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1504 TATAAGATAATAAGCAAGCTTGACTCAAAACAGCCAAATTTGAAGTCTTACCTAACCA 1563
QY 661 AAG 663
Db 1564 AAG 1566

RESULT 3

US-08-526-840B-33
; Sequence 33, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:

; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.

; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND

; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY

Handwritten notes: "noted" and "1158 to 1578" with a circle around the sequence range.

QY 1 CAACAGACCCGATCCAGCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 60
DB |||||
QY 904 CAACAGACCCGATCCAGCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 963
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DB |||||
QY 964 ATATATTTTCTTTATGAGGGTGACCTGTTACTCAGAGAATGTGAATCTCTGATCAA 1023
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DB |||||
QY 1024 CTTAGATCTCAGGATTAATATATATGTTTTCAGGGCCAAATATGATAAAATTAATAACT 1083
DB |||||
QY 181 GAACTTAACCAACAGAGATGCAACTTTATTTAGGATAAAAGCTTGATATTTATGTT 240
DB |||||
QY 1084 GAACTTTAAGAACCAAGAGATGCAACTTTATTTAGGATAAAAGCTTGATATTTATGTT 1143
DB |||||
QY 241 GTAGAAATTTACCATCTCTGTTTATTTATGTAAGAAATGCAGAAAGGAGTGCAATCTATAC 300
DB |||||
QY 1144 GTAGAAATTTACCATCTCTGTTTATTTATGTAAGAAATGCAGAAAGGAGTGCAATCTATAC 1203
DB |||||
QY 301 GGAGGGGTAAACAAATCATGAGGGAATCAATTTAGAAATTCCTAAAAGATGTCGTTAAA 360
DB |||||
QY 1204 GGAGGGGTAAACAAATCATGAGGGAATCAATTTAGAAATTCCTAAAAGATGTCGTTAAA 1263
DB |||||
QY 361 GPATCAATCGATGGTATCCAAAGCCTATCATTTGATATTTGAAACAAATTAATAAAATGGTA 420
DB |||||
QY 1264 GPATCAATCGATGGTATCCAAAGCCTATCATTTGATATTTGAAACAAATTAATAAAATGGTA 1323
DB |||||
QY 421 ACTGCTCAAGAAATAGACTATATAAGTTAGAAATATCTTACAGATAATAAGCAACTATAT 480
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QY 1324 ACTGCTCAAGAAATAGACTATATAAGTTAGAAATATCTTACAGATAATAAGCAACTATAT 1383
DB |||||
QY 481 ACTAATGACCTTCAATATGAAAGCTGATATATAAGTTACATCTAAAGATTAAGAA 540
DB |||||
QY 1384 ACTAATGACCTTCAATATGAAAGCTGATATATAAGTTACATCTAAAGATTAAGAA 1443
DB |||||
QY 541 AGTTTGTGTTGATTTTTCCTGAAACAGAAATTTACTCAATCTAAATCTTATGATA 600
DB |||||
QY 1444 AGTTTGTGTTGATTTTTCCTGAAACAGAAATTTACTCAATCTAAATCTTATGATA 1503
DB |||||
QY 601 TATAAGATAATGAAAGCTTGACTCAACACAAAGCCAAATTTGAAGTCTACCTAACCAACC 660
DB |||||
QY 1504 TATAAGATAATGAAAGCTTGACTCAACACAAAGCCAAATTTGAAGTCTACCTAACCAACC 1563
DB |||||
QY 661 AAG 663
DB 1564 AAG 1566

RESULT 5

US-08-446-918A-1
; Sequence 1, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,918A
; FILING DATE: 18-MAY-1995

RESULT 6

US-08-580-806-1
; Sequence 1, Application US/08580806
; Patent No. 5935568

CLASSIFICATION: 552
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 773 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: CDS
LOCATION: 1..768
US-08-446-918A-1

Query Match 25.2%; Score 166.8; DB 1; Length 773;
Best Local Similarity 59.1%; Pred. No. 9.4e-30;
Matches 384; Conservative 0; Mismatches 221; Indels 45; Gaps 4;
QY 56 AAAATATATATTTCTTTATGAGGGTGACCTGTTACTCACGAGAATGTGAATCTGTG 115
DB |||||
QY 113 AAAATATGAAAGTTTGTATGATGATATCAATGATATGATATGATATGATATGATATGAT 172
DB |||||
QY 116 ATCAACTTTTATCTCACCATTTAATATATATATATATATATATATATATATATATATATG 166
DB |||||
QY 173 ATCAATTTCTATCTTACCTTATATATATATATATATATATATATATATATATATATATG 232
DB |||||
QY 167 ATAAATTAATAACTGAACTTAAGAACCAAGAGATGGCACTTATTTAAGGATATAAAGCG 226
DB |||||
QY 233 ATAATGTTGAGTGGCAATTTTAAAAACAAAGATTTAGCTGATATAATACAAAGATAAATACG 292
DB |||||
QY 227 TTGATATTTATGTTGTAGAAATATATACCATCTCTGTTATTTATGTCGAAA- 275
DB |||||
QY 293 TAGATGTTGAGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 352
DB |||||
QY 276 TGCAGAAAGGAGTGCAATGATCTTACGGAGGGGTAAACAAATCATG 319
DB |||||
QY 353 TTAAATTCGCATCAAACTGACAAACGAAACCTTGATGATGATGATGATGATGATGATGATGATG 412
DB |||||
QY 320 AAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCTGTTAAAGTATCAATCGATGTTATCC 379
DB |||||
QY 413 ATGGAACCAATATAGATAATATAGAGTATTTACTGTTGCGGTATTTGGAAGATGGTAAAA 472
DB |||||
QY 380 AAAGCTATCATTTGATATGAAACAAATTAATAATATGTTAACTGCTCAAGAAATTAGACT 439
DB |||||
QY 473 ATTTATTTCTTTGACGTACAACTAATAGAAAAGGTGATGCTGCTCAAGAAATTAGATT 532
DB |||||
QY 440 ATAAAGTTAGAAAATATCTTACAGATAATAAGCAACTATATATACTAATGGAACCTTCTAAAT 499
DB |||||
QY 533 ACCTAACTCGTCACATTTTGGTGAATAATAAAAACTCTATGAATTAACCAACTCGCCTT 592
DB |||||
QY 500 ATGAACTGGATATATAAGTTCACTACCAAGATAAGAAAGATTTTGGTTGATTTT 559
DB |||||
QY 593 ATGAAACGGATATATATAATTTATA---GAAAAAGAGAATAGCTTTTGGTATGACATGA 649
DB |||||
QY 560 TCCCTGAAACCGAG- - - - - AATTTACTCAATCTAAATATCTTATGATATATAAGATAATG 613
DB |||||
QY 650 TGCCTGCAACCGAGGAGATTAATTTGACCAATCTAATATATTTAATGATGATACATGACATA 709
DB |||||
QY 614 AAACGTTGACTCAAAACACAAAGCCAAATTTGAAGTCTTACCTAACCAACCAAG 663
DB |||||
QY 710 AAATGTTGATTTCTAAAGATGTGAAGATTTGAAGTTTATCTTACGACAAG 759
DB |||||

GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
APPLICANT: Potter, Terence A.
TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 773 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: CDS
LOCATION: 1..768
US-08-580-806-1

Query Match 25.2%; Score 166.8; DB 2; Length 773;
Best Local Similarity 59.1%; Pred. No. 9.4e-30;
Matches 384; Conservative 0; Mismatches 221; Indels 45; Gaps 4;

QY 56 ABAATATATATTTCTTTATGAGGGTGACCTGTACTCAGGAAATGTGAATCTCTTG 115
DB 113 ABAATATGAAAGTTTGTATGATGATAATCATGTATCAGCAATAAAGCTTAAATCTATAG 172

QY 116 ATCAACTTTTATCTCACCATTTAATATATATATGTTTCAGGGCCA-----AATTATG 166
DB 173 ATCAATTTCTATCTTTGACCTTAATATATCTATTAAGGACACTAAGTTAGGGAATTATG 232

QY 167 ATAAATTAAGTAACTTAAGAACCAAGAGATGGCACTTTATTTAAGGATAAAACG 226
DB 233 ATAAATGTCAGTGAATTTAAACCAAGATTAGCTGATATAACAGATAAATACG 292

QY 227 TTGATATTATGTTGATAGATATTAACATCTGTTTATTTATGTGAAA----- 275
DB 293 TAGATGTTTGGAGCTTAATTTATTTATTAATCAATGTTATTTCTTAAACCAAGATGATA 352

QY 276 -----TGCAGAAAGGAGTCAATGATCTACGGAGGGGTACAAATCATG 319
DB 353 TTAATTCGCATCAAACTGACAAACGAAACCTTGATGTTGTTGGGTGAGTAACTGAGATA 412

QY 320 AAGGAATCATTTAGAAATTTCTTAAAGATAGTCGTTAAAGTATCAATCGATGGTATCC 379
DB 413 ATGAAACCAATTAGATAAATAGAGATTAATCTGTTCCGGTATTTGAGATGGTAATA 472

QY 380 AAGCCATCATTTGATTTGAACCAATTAATAAATATGTTAACTGCTCAAGATTTAGACT 439
DB 473 ATTTATTTATCTTTTGACGTACAACTAATAAGAAAAAGGTGACTGCTCAAGAAATTAGATT 532

QY 440 ATAAAGTTAGAAATATCTTACAGATAATAAGCAACTATATATACTAAATGCGACCTTCTAAAT 499
DB 533 ACCTAACTCGTCACTATTGGTGAAAAATAAAAACTCTATGAATTTTAAACAACCTGCGCTT 592

QY 500 ATGAAACTGGATATATAAAGTTTACCTAAGATAAAGAAAGTTTGGTTGATTTT 559
DB 593 ATGAAACGGGATATATAATTTATA---GAAATGAGATAGCTTTTGGTATGACATGA 649

QY 560 TCCCTGAACCCAG-----AATTTACTCAATCTAAATATCTTATGATATATAAAGATAATG 613
DB 650 TGCCTGCACCCAGGAGATAAATTTGACCAATCTAAATATTTAATGATGTACAAATGACAATA 709

QY 614 AAACGCTTGACTCAAAACACAGCCAAATTTGAAGTCTACCTAACCAACCAAG 663
DB 710 AATGGTTGATTTCTAAAGATGTGAAGATTGAAGTTTATCTTACGACCAAG 759

RESULT 7
US-144-776B-5
Sequence 5, Application US/09144776B
Patent No. 6399332
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1712
TYPE: Nucleic Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-144-776B-5

Query Match 25.2%; Score 166.8; DB 4; Length 1712;
Best Local Similarity 59.1%; Pred. No. 1.1e-29;
Matches 384; Conservative 0; Mismatches 221; Indels 45; Gaps 4;

QY 56 AAAAAATATATTTTCTTTATGAGGGTGACCTGTACTCAGGAGAAATGTGAATCTGTTG 115
DB 389 AAGATATGAAAGTTTGTATGATGATAATCATGATCAAGCAATAAAGCTTAAATCTATAG 448

; APPLICANT: Lee, John Scott
 ; APPLICANT: Pushko, Peter
 ; APPLICANT: Smith, Jonathan F.
 ; APPLICANT: Ulrich, Robert G.
 ; TITLE OF INVENTION: Vaccine Against Staphylococcus Intoxication
 ; FILE REFERENCE: Army-136
 ; CURRENT APPLICATION NUMBER: US/09/350,755A
 ; CURRENT FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: US 60/092,416
 ; PRIOR FILING DATE: 1998-07-10
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: Microsoft Word 97 (IBM compatible)
 ; SEQ ID NO 3
 ; LENGTH: 723
 ; TYPE: DNA
 ; ORGANISM: Staphylococcus aureus
 US-09-350-755A-3

Query Match 24.0%; Score 158.8; DB 4; Length 723;
 Best Local Similarity 58.3%; Pred. No. 6.4e-28;
 Matches 379; Conservative 0; Mismatches 226; Indels 45; Gaps 4;

```

Qy 56 AAAATATATATTTCTTTATGAGGGTGACCTGTCTACACGAGAATGTGAATCTGTG 115
Db 68 AAAATATGAAAGTTTGTATGATGATATATATCTATCAGCAATAAACGTTAACTATAG 127

Qy 116 ATCAACTTTTATCTCACCATTTAATATATATATGTTTCAGGGCCA-----AATTATG 166
Db 128 ATCAATTTGATCTTTGACTTTAATATATCTTAAAGGACACTAAGTTAGGGAATTATG 187

Qy 167 ATAAATTAATAAAGTAAAGTAAAGGAGATGGCAACTTTAATTAAGGATATAAACG 226
Db 188 ATAATGTTGAGTCGAATTTAAACAAGATTTAGCTGATAAATACAAAGATATAACG 247

Qy 227 TTGATATTTATGGTGTAGAAATATACCATCTCTGTTATTTATGTAAGGAAAA 275
Db 248 TAGATGTTTGGAGCTAAATCTTATTAATCAATGTCCTTTTCTAAAGGAAACGAATGATA 307

Qy 276 -----TGCAGAAAGGAGTGATGATCTACGAGGGGTAACAATCATG 319
Db 308 TTAATTCGCATCAAACTGACAAACGAAACCTTGTATGATGGTGGTAACTGAGCATA 367

Qy 320 AAGGGAATCATTTAGAAATCTTAAAGAGATAGTCGTTAAAGTATCAATCGATGATCC 379
Db 368 ATGGAACCAATTAGATAAATATAGAGTATCTGTTGCGGTAATTTGAAGATGTAATA 427

Qy 380 AAGCCTATCATTTGATATGAAACAAATAAATAAATGGTAACCTGCTCAAGAAATTAGACT 439
Db 428 ATTATTTATCTTTTGACGTACAACTAATAAGAAAAAGGTGACTGCTCAAGAAATTAGATT 487

Qy 440 ATAAAGTTAGAAATATCTTACAGATAATAGCAACTATATCTAATGGACCTTCTAAAT 499
Db 488 ACCTAATCTGTCATTTTGGTGAAATAAATAAATAAATCTATGAATTTAAACAACFCGCTT 547

Qy 500 ATGAACTGGATATATAAGTTCTACCTAAGATAAAGAAAGTTTGTGTTGATTTT 559
Db 548 ATGAAACGGGATATATAAATTATA---GAAATGAGATAGCTTTTGGTATGACATGA 604

Qy 560 TCCTGAAACGAG-----AATTACTCAATCTAAATCTTATGATATATAAAGATAATG 613
Db 605 TGCTGCACGAGGAGATAAATTTGACCAATCTAAATTTAATGATGATGATGACATA 664

Qy 614 AAGCGTTGACTCAACACAGCCAAATTTGAGTCTACCTACCTAAACCAACG 663
Db 665 AATGGTGTATCTTAAAGATGTGAAGATTGAAGTTTATCTTACGACAAAG 714
  
```

RESULT 10
 US-09-350-755A-2
 ; Sequence 2, Application US/09350755A
 ; Patent No. 6632640
 ; GENERAL INFORMATION:
 ; APPLICANT: United States Army Medical Research Institute of Infectious Diseases

; APPLICANT: Lee, John Scott
 ; APPLICANT: Pushko, Peter
 ; APPLICANT: Smith, Jonathan F.
 ; APPLICANT: Ulrich, Robert G.
 ; TITLE OF INVENTION: Vaccine Against Staphylococcus Intoxication
 ; FILE REFERENCE: Army-136
 ; CURRENT APPLICATION NUMBER: US/09/350,755A
 ; CURRENT FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: US 60/092,416
 ; PRIOR FILING DATE: 1998-07-10
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: Microsoft Word 97 (IBM compatible)
 ; SEQ ID NO 2
 ; LENGTH: 801
 ; TYPE: DNA
 ; ORGANISM: Staphylococcus aureus
 US-09-350-755A-2

Query Match 24.0%; Score 158.8; DB 4; Length 801;
 Best Local Similarity 58.3%; Pred. No. 6.6e-28;
 Matches 379; Conservative 0; Mismatches 226; Indels 45; Gaps 4;

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Qy 56 AAAATATATATTTCTTTATGAGGGTGACCTGTCTACGAGAATGTGAATCTGTG 115
Db 146 AAAATATGAAAGTTTGTATGATGATATCTAATGATCAGCAATAAACGTTAACTATAG 205

Qy 116 ATCAACTTTTATCTCACCATTTAATATATATATGTTTCAGGGCCA-----AATTATG 166
Db 206 ATCAATTTGATCTTTGACTTTAATATATCTTAAAGGACACTAAGTTAGGGAATTATG 265

Qy 167 ATAAATTAATAAAGTAAAGTAAAGGAGATGGCAACTTTAATTAAGGATATAAACG 226
Db 266 ATAATGTTGAGTCGAATTTAAACAAGATTTAGCTGATAAATACAAAGATATAACG 325

Qy 227 TTGATATTTATGGTGTAGAAATATACCATCTCTGTTATTTATGTAAGGAAAA 275
Db 326 TAGATGTTTGGAGCTAAATCTTATTAATCAATGTCCTTTTCTAAAGGAAACGAATGATA 385

Qy 276 -----TGCAGAAAGGAGTGATGATCTACGAGGGGTAACAATCATG 319
Db 386 TTAATTCGCATCAAACTGACAAACGAAACCTTGTATGATGGTGGTAACTGAGCATA 445

Qy 320 AAGGGAATCATTTAGAAATCTTAAAGAGATAGTCGTTAAAGTATCAATCGATGATCC 379
Db 446 ATGGAACCAATTAGATAAATATAGAGTATCTGTTGCGGTAATTTGAAGATGTAATA 505

Qy 380 AAGCCTATCATTTGATATGAAACAAATAAATAAATGGTAACCTGCTCAAGAAATTAGACT 439
Db 506 ATTATTTATCTTTTGACGTACAACTAATAAGAAAAAGGTGACTGCTCAAGAAATTAGATT 565

Qy 440 ATAAAGTTAGAAATATCTTACAGATAATAGCAACTATATCTAATGGACCTTCTAAAT 499
Db 566 ACCTAATCTGTCATTTTGGTGAAATAAATAAATAAATCTATGAATTTAAACAACFCGCTT 625

Qy 500 ATGAACTGGATATATAAGTTCTACCTAAGATAAAGAAAGTTTGTGTTGATTTT 559
Db 626 ATGAAACGGGATATATAAATTATA---GAAATGAGATAGCTTTTGGTATGACATGA 682

Qy 560 TCCTGAAACGAG-----AATTACTCAATCTAAATCTTATGATATATAAAGATAATG 613
Db 683 TGCTGCACGAGGAGATAAATTTGACCAATCTAAATTTAATGATGATGATGACATA 742

Qy 614 AAGCGTTGACTCAACACAGCCAAATTTGAGTCTACCTACCTAAACCAACG 663
Db 743 AATGGTGTATCTTAAAGATGTGAAGATTGAAGTTTATCTTACGACAAAG 792
  
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RESULT 11
 US-09-144-776B-9
 ; Sequence 9, Application US/09144776B
 ; Patent No. 6399332
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,

Db	425	ATTATATATCTTTTGACGTACAACTAATAAGAAAAAGCTGACTGCTCAAGBATTAGATT	481
Qy	440	ATAAGTTAGAAAATATCTTACAGATAATAAGCAACTATATATCTAATGACCTTCTAAAT	499
Db	485	ACCTAACTCGTCACTATTGGTGAATAATAAAAACTCTATGAATTTTAACTACGCTT	544
Qy	500	ATGAACTGGATATATAAAGTTTCATACCTAAGATAAAGAAAGTTTTCGTTTGATTTT	559
Db	545	ATGAAACGGGATATATTAATTTATA---GAAATGGAATAGCTTTTGTATGACATGA	601
Qy	560	TCCTGAAACGAG-----AATTTACTCAATCTAAATATCTTATGATATATAAGATAATG	613
Db	602	TGCTGCACCGAGAGATAATTTGACCAATCTAAATATTTAATGATGTACATGACAAATA	661
Qy	614	AAACGTTGACTCAACACAGCCAAATTTGAAGTCTTACTTACCAACCAAG	663
Db	662	AAATGGTTGATTCTTAAAGATGTGAAGATTGAAGTTTATCTTACGACAAAG	711
RESULT 12			
US-09-144-776B-7			
; Sequence 7, Application US/09144776B			
; Patent No. 639332			
; GENERAL INFORMATION:			
; APPLICANT: Robert G. Ulrich,			
; Sina Bavari			
; TITLE OF INVENTION: Bacterial Superantigen			
; Vaccines			
; NUMBER OF SEQUENCES: 25			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Charles H. Harris			
; STREET: US Army MRC -504 Scott Street			
; MCMR-JA (Charles H. Harris-Patent			
; Atty)			
; CITY: FORT DETRICK			
; STATE: MARYLAND			
; COUNTRY: USA			
; ZIP: 21702-5012			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: Apple Macintosh			
; OPERATING SYSTEM: Macintosh 7.5			
; SOFTWARE: Microsoft Word 6.0			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/144,776B			
; FILING DATE: 01-Sep-1998			
; CLASSIFICATION: <Unknown>			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/882,431			
; FILING DATE: <Unknown>			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Charles H. Harris			
; REGISTRATION NUMBER: 34,616			
; REFERENCE/DOCKET NUMBER: <Unknown>			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (301) 619-2065			
; TELEFAX: (301) 619-7714			
; INFORMATION FOR SEQ ID NO: 9:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1388			
; TYPE: Nucleic Acid			
; STRANDEDNESS: Unknown			
; TOPOLOGY: Unknown			
; MOLECULE TYPE: DNA			
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:			
US-09-144-776B-9			
Query Match 24.0%; Score 158.8; DB 4; Length 1388;			
Best Local Similarity 58.3%; Pred. No. 7.4e-28;			
Matches 379; Conservative 0; Mismatches 226; Indels 45; Gaps 4;			
Qy	56	AAAATATATATTTCTTTATGAGGGTGACCTGTTACTCAGAGAAATGTGAATCTGTG	115
Db	65	AAAATATGAAGTTTGTATGATGATAATCATGTATCAGCAATAAAGTTAAATCTATAG	124
Qy	116	ATCAACTTTTATCTCACCATTATATATAATGTTTCAGGCGCA-----AATTATG	166
Db	125	ATCAATTCGATCTTTGACTTAATATATCTTATTAAGACACATAGTTAGGGAATTATG	184
Qy	167	ATAAATTAATAAAGCTGAACCTTAAGAACAAGAGATGCGCACTTTTATTAAGGATAAAGCG	226
Db	185	ATAATGTCGAGTCGAATTTAAAAACAAGATTAGCTGATATAAACAAGATAAATACG	244
Qy	227	TTGATATTTAGGTGATAGATATATACCATCTCTGTTATTTATCTGAAA-----	275
Db	245	TAGATGTGTTGGAGCTAAATGCTTTATATCAATGTGCTTTTCTAAAAAACAAGATGA	304
Qy	276	-----TGCAAGAAGGAGTGCATGTATCTACGGAGGGGTAAACAAATCATG	319
Db	305	TTAATTCGCATCAAACTGACAAACGAAAACTTGTATGATGTTGGTGAATCTGACATA	364
Qy	320	AAGGAATCATTTAGAAATTCCTTAAAGATAGCTGTTAAAGTATCAATCGATGGTATCC	379
Db	365	ATGGAACCAATATAGATAAATAAGAGTATTAATCTGTTGGGTATTTGAAGATGGTAAA	424
Qy	380		

[illegible]

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RESULT 13
US-09-414-276-7
; Sequence 7, Application US/09414276
; Patent No. 6392121
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh
; APPLICANT: Palmer, Kenneth
; APPLICANT: Hefferon, Kathleen
; APPLICANT: Mor, Tsafir
; APPLICANT: Antzen, Charles
; TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
; FILE REFERENCE: 4869/84453
; CURRENT APPLICATION NUMBER: US/09/414,276
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 815
; TYPE: DNA
; ORGANISM: bean yellow dwarf virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(803)
US-09-414-276-7

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Query Match 16.9%; Score 112; DB 4; Length 815;
Best Local Similarity 58.8%; Pred. No. 3.8e-17;
Matches 234; Conservative 0; Mismatches 155; Indels 9; Gaps 2

Qy	272	AAATGCAAGAAAGGAGTGCAATGTAATCTACGAGGGGTAAACAAATCATGAAGGGAATCATTT	331
Db	400	AAACTGACACAGAGAAAGACTTGCATGTATGGTGGTGACTGAGCACAAACGGAACCAAT	459
Qy	332	TAGAAATTCCTAAAAGNATAGTCGTTTAAAGTATCAATCGATGGTATCCAAAGCCTTATCAT	391
Db	460	TGGACAATATCAGGAGCATCTGTGAGGGTGTGAGGATGGTAAGAACCTCCTCTCTT	519
Qy	392	TTGATATTGAAACAAATAAAAAATGGTAACTGCTCAAGAATTAGACTATAAAGTTAGAA	451
Db	520	TTGATGTGCAAACTAACAGAGAGAGGTGACTGCTCAAGAGTTGAGCTACCTACCTAGGC	579
Qy	452	AATATCTTACAGATAATAAGCAACTATATACATAATGSGACCTTCTAAATATGAAACTGGAT	511
Db	580	ACTACTTGGTGAAGAACAGAGAAGCTCTATGAGTTCAACAACAGACCCCTTATGAGACTGGAT	639
Qy	512	ATATAAGTTTCATACCTTAAGNATAAGNAAAGTTTTTGGTTTGAATTTTTTCCCTGAACCAAG	571
Db	640	ACATCAAGTTTCAT---TGAGAAATGAGAACACGCTTCTGGTATGACATGATGCTCGCACCAG	696
Qy	572	-----AATTTTACTCAATCTAAATATCTTATGATATATAAAGATAATGAAACGCTTGACT	625
Db	697	GAGACAAGTTTGACCAATCTAAGTACCTCATGATGTACATATGACAAAGATGGTGACT	756
Qy	626	CAACACAAGCCAAATTGAAGTCTACCTTAACAACCAAG	663
Db	757	CTAAGGATGTGAAGATTGAGGTGTACCTTACCACCAAG	794
RESULT 14			
US-09-144-776B-3			
; Sequence 3, Application US/09144776B			
; Patent No. 6399332			
; GENERAL INFORMATION:			
; APPLICANT: Robert G. Ulrich,			
; Mark A. Olson			
; Sina Bavari			
; TITLE OF INVENTION: Bacterial Superantigen			
; Vaccines			
; NUMBER OF SEQUENCES: 25			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Charles H. Harris			
; STREET: US Army MRCM -504 Scott Street			
; MCMR-JA (Charles H. Harris-Patent			
; Atty)			
; CITY: FORT DETRICK			
; STATE: MARYLAND			
; COUNTRY: USA			
; ZIP: 21702-5012			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: Apple Macintosh			
; OPERATING SYSTEM: Macintosh 7.5			
; SOFTWARE: Microsoft Word 6.0			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/144,776B			
; FILING DATE: 01-Sep-1998			
; CLASSIFICATION: <Unknown>			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/882,431			
; FILING DATE: <Unknown>			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Charles H. Harris			
; REGISTRATION NUMBER: 34,616			
; REFERENCE/DOCKET NUMBER: <Unknown>			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (301) 619-2065			
; TELEFAX: (301) 619-7714			
; INFORMATION FOR SEQ ID NO: 3:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 757			
; TYPE: Nucleic Acid			
; STRANDEDNESS: Unknown			

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;      TOPOLOGY: Unknown
;      MOLECULE TYPE: DNA
;      SEQUENCE DESCRIPTION:
US-09-144-776B-3

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Query Match	10.7%;	Score 71;	DB 4;	Length 757;
Best local Similarity	47.8%;	Pred. No. 1e-07;		
Matches 311;	Conservative 0;	Mismatches 325;	Indels 15;	Gaps 3;
QY	23	AAC TTCACAGATCTAGT TTTAGT TTA AAAACCTTCAA AATATATATATTTCTTTATGAGGGTG	82	
DB	49	AA TTGCAGGAAACAGCTTTAGGCAATCTTAAACAAATCTATTATTACAAATCAAAAAGCTA	108	
QY	83	ACCTGTTTACTCAGAGAAATGTGAAATCTGTTGATCAAACTTTTATCTCAACATTTAAATAT	142	
DB	109	AAACTGAAAAATAAAGAGAGAGTCACGATCAATTTTCGACAGCACTATATTTGTTTAAAGGCT	168	
QY	143	ATAATGTTTCAGGGCCAAAATTATCATAAATTTAAAAAACTGAACTTAAAGAACCAACAGATGG	202	
DB	169	TTTTTACAGATCATTCGTGGTATAAACGATTTATTAGTACGTTTTCATTCAAAGATATTG	228	
QY	203	CAACTTTATTAAAGATAAAAACGTTTGATATTATATGGTGTAGAATAATTACCATCTCTGTT	262	
DB	229	TTGATAAATATAAAGGGA AAAAAGCTAGACTTGTATGTGTCTTATCTGCTGTTATCAATG--	286	
QY	263	ATTTTATCTGAAATTCGCAAGAGAGTGCATGCTATCTACGGAGGGGTAAACAAATCATGAAG	322	
DB	287	-TGGGGTGGTACACCAACAAAACAGCTTGATGTATGGTGGTGTACGTTACATGATA	345	
QY	323	GGAATCATTTAGAAATTCCTAAAAAGATAGTTCGTTAAAGTATCAATCGATGGTATCCAAA	382	
DB	346	ATAATCGATTGACCGAAGAGAAAAAGTGC CGATCAATTTATGGCTAGACGGTAAACAAA	405	
QY	383	GCCTATCATTTGA-----TATTGAACAAATAAAAAAATCGTAACTGCTCAAGAAATTAG	436	
DB	406	ATACAGTACCTTTGCGAAACGGTTTAAACGAAATAAGAAAAATGTAACTGTTTCAGAGATTG	465	
QY	437	ACTATAAGTTTAGAAAAATATCTTACAGATAATAAGCAACTATATACTAAATCGACTTCT-	495	
DB	466	ATCTTCAAGCAAGAGCTTTATTACAGGAAAAATAATATTATATAAATCTCGATGTTTWTG	525	
QY	496	-----AAATATGAACCTGGATATATAAGTTTCATACCTTAAGAAATAAGAAAAGTTTGGT	550	
DB	526	ATGGGAAGGTTTCAGAGGGGATTAATTCGTGTTTCATCTTCTACAGAAACCTTCGGTTAAT	585	
QY	551	TTGATTTTTTCCCTGAACCAAGATTTACTCAATCTAAATATCTTATGATATATAAAGATA	610	
DB	586	ACGATTTATTITGGTGCTCAAGGACAGTATTCAAATACACTATTAGAATATATAGATA	645	
QY	611	ATGAACGCTTTGACTCAACACAAGCCAAAATTGAAGTCTACCTAACACCA	661	
DB	646	ATAAAACGATTAACTCTGAAACATGCGATAATTGATATATATTTATATATACAA	696	

RESULT 15

```

US-09-350-755A-1
; Sequence 1, Application US/09350755A
; Patent No. 6632640
; GENERAL INFORMATION:
; APPLICANT: United States Army Medical Research Institute of Infectious Diseases
; APPLICANT: Lee, John Scott
; APPLICANT: Pushko, Peter
; APPLICANT: Smith, Jonathan F.
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Vaccine Against Staphylococcus Intoxication
; FILE REFERENCE: Army-136
; CURRENT APPLICATION NUMBER: US/09/350,755A
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/092,416
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 97 (IBM compatible)
; SEQ ID NO 1

```

; LENGTH: 757
 ; TYPE: DNA
 ; ORGANISM: S
 US-09-350-755A-

Query Match	10.7%	Score 71	DB 4	Length 757
Best Local Similarity	47.9%	Pred. No. 1e-07		
Matches 311	Conservative 0	Mismatches 325	Indels 15	Gaps 3
Qy	23	AACTTCACAGACTAGTTTAAAGTTTAAACACCTTCAAAATATATATTTTCTTTATGAGGGTG	82	
Db	49	AAATGTCAGGAAACAGCTTTAGGCAATCTTAAACAAATCTATTATACAATGAAAAAGCTA	108	
Qy	83	ACCTGTTATCTCAGAGAAATGTGAATCTGTTGATCAACTTTTATCTCACCATTTAATAT	142	
Db	109	AAACTGAAAAATAAGAGAGAGTCAGCAGTCAATTTTCGACAGCATCTATATGTTTAAAGCGT	169	
Qy	143	ATAATGTTTCAGGGCCAAATTTATGATAAATATAAAAACTGAACTTAAGAACCAAGAGATGG	203	
Db	169	TTTTTACAGATCATTCGTGGTATAACGATTTATAGTACGTTTGAATCAAGGATATTG	228	
Qy	203	CAACTTTATTTAAGGATAAAAAAGTTGATATTTATATGTTGATAGAAATATACCACTCTCTGTT	262	
Db	229	TTGATTAATATAAAGGGAAAAAGTAGTACATGTGATGTTGCTTATGCTGGTTATCAATG--	286	
Qy	263	ATTATGTGAAATGCGAAGAGGAGTCATGTATCTACGAGGGGTAAACAAATCATCAAG	322	
Db	287	TGGGGTGGTACACCAAACAAACAGCTTGTATGTATGTTGGTGTAAACGTTACATGATA	345	
Qy	323	GGATCATTTAGAAATTCCTAAAAAGATAGTCGTTAAAGTATCAATCGATGGTATCCAAA	382	
Db	346	ATAATCGATTTGACCGAAGAGAAAAAAGTCGGCATCAATTTATGCTAGACGGTAAACAAA	405	
Qy	383	GCCTATCATTTGA-----TATTGAAACAAATAAAAAAGTAACTGCTCAAGAATTAG	436	
Db	406	ATACAGTACCTTTGGAAACGGTTAAAAACGAATAGAAAAATGTAACTGTTTCAGAGATTG	465	
Qy	437	ACTATAAGTTAGAAAAATATCTTACAGATAATAGCAACTATATPACTAATGGACCTTCT-	495	
Db	466	ATCTTCAAGCAAGCGTTATTTCAGGAAAAATATAATTTATATACTCTGATGTTTTTG	525	
Qy	496	-----AAATATGAACTGGATATAATAAGTTTCATCCTAAGATAAAGAAAGTTTTCGT	550	
Db	526	ATGGGAAGGTTTCAGAGGGGATTAATCGTTTTCATCTCTACAGAACCTTCGGTTAATT	585	
Qy	551	TTGATTTTTTCCCTGAAACCAGAAATTTACTCAATCTAAATATCTTATGATATATAAGATA	610	
Db	586	ACGATTTATTGGTGTCTCAGGACAGTATTCAAATACACTATTAAAGATATATAGATA	645	
Qy	611	ATGAAACGCTTGACTCAAAACAAAGCCAAATTTGAAGTCTCACTTAACACCA	661	
Db	646	ATAAAGCATTAACCTCTGAAACATGATATGATATATATATATATATATATATACAA	696	

Search completed: September 3, 2004, 18:58:10
Job time : 82 secs

	Query Match	Best Local Similarity	2.1%;	Score 39,000;	DB 1;	Length 1114;
	Matches 123;	Conservative	46.8%;	Pred No 0.005;		
				Mismatches 140;	Indels 0;	Gaps 0;
597	ATATATAACATATTTTCATCCTCTACCTACTTACTTCGTAAAGATATAAAATACTATTG					656
799	ATAAATCAGAAATATGTGATCATCAAGCATCTCTGTAATTTATTATAAATAAATCAATTC					740
657	TTTTTTTTTGTATTTTATATAAATAATTTATAATATAGTTTAATGTTTTTAAAAATATAC					716


```

; APPLICANT: QUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY
; TITLE OF INVENTION: DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY
; TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
; TITLE OF INVENTION: LABORATORY
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,732B
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
;
; US-08-304-732B-31
;
; Query Match
; Best Local Similarity 1.5%; Score 29.4; DB 1; Length 3754;
; Matches 75; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
;
; QY 652 TATGTTTTTTTGTATTTATTAATAAATTAATAATAAGTTAATGTTTATTTTAAAAA 711
; DB 339 TTGGACTTTTCTACTATTTATCAATTTTAAAGAGAGAGAAAAATTTTGAATC 398
;
; QY 712 TATCAATTTTATCTATTATAGTAGTAGCTATTTTTCATTTCTAGTAAATTTGGTGAAT 771
; DB 399 TCTGTGTTTTTGGTAAATATGTTTAAATATATAGTTTAAATATAGTTTAAATATGTC 458
;
; QY 772 TGTATACCTTTTAAATCTAGAGGAGAAC 802
; DB 459 ACGAAGAGAGATTTTATGAGAGAGAGATC 489
;
; RESULT 5
; US-08-304-732B-35
; Sequence 35, Application US/08304732B
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: QUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY
; TITLE OF INVENTION: DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY
; TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
; TITLE OF INVENTION: LABORATORY
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,732B
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5953 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Lactococcus lactis
;
; US-08-304-732B-35
;
; Query Match
; Best Local Similarity 1.5%; Score 28.6; DB 1; Length 5953;
; Matches 91; Conservative 0; Mismatches 84; Indels 4; Gaps 1;
;
; QY 697 AATGTTTTTTTAAATATACATTTTATCTATTATAGTAGCTATTTTTCATTTGTA 756
; DB 47 AATAAATAAAGAGAGATTTCAATTTTCTATTATATAAAAAATTTAGTTAAGTTAA 106
;
; QY 757 ----GTAATATGTTGTAATTAACCTTTTAAATCTAGAGGAGAACCATATAA 812
; DB 107 AACATCATTTCTACGTAAAAATCAAGAAATTTTATCTCATAGGTAAAGAGACTAAA 166
;
; QY 813 AATGGAGGATATTTATGGAACATATAAAGATTTTGAAGAAATGTTATTTTGT 871
; DB 167 ATAAGCACCTTATCTTTATTTAAAGAAAGCAAGCTTAAAAAGAGACTAATTTT 225
;
; RESULT 6
; US-08-304-732B-24
; Sequence 24, Application US/08304732B
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: QUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY
; TITLE OF INVENTION: DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY
; TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
; TITLE OF INVENTION: LABORATORY
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```


APPLICATION NUMBER: US/08/304,732B
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: *Staphylococcus saprophyticus*
US-08-304-732B-24

Query Match
Best Local Similarity 1.5%; Score 27.5; DB 1; Length 258;
Matches 106; Conservative 0; Mismatches 110; Indels 5; Gaps 1;
QY 515 AAATATCTTCGGTTTTAGCCACTATCGCTACTGTGTCACCTAAATATACCCCTTATC 574
DB 10 AATTACATTCGGCTCATTCAGTACAGTGCAGATCGGTCAGATAGTTCTCTCGTTAGC 69
QY 575 AATGCTCTTTTAACTCATCTATATATACATATTC-----ATCCCTCTACCTACTA 629
DB 70 TTGACTCTTAACTATCTGTCTAAATTTGTTTATCTTCTGATCTGACTAGAAATTTA 129
QY 630 TCGTAAAGATAAAATACATATGTTTTTTTGTATTTATTAATAAATATTATTAAT 689
DB 130 CTCTAATCTCTGATTCATATTCATCTGATTCATATATATATATATATATATTTG 189
QY 690 ATAAGTTAATGTTTTTAAATATATACATTTTATCTATT 730
DB 190 ATGAATCTTGTATCTGACATACAGGAGTGTCTCATT 230

RESULT 7
US-08-304-732B-27
Sequence 27, Application US/08304732B
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY
TITLE OF INVENTION: DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY
TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,732B
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1817 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 9100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: *Haemophilus influenzae*
US-08-304-732B-27
Query Match
Best Local Similarity 1.5%; Score 27; DB 1; Length 9100;
Matches 63; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 668 ATTTTATAAAAAATTATTATATAAGTTAATGTTTTTTTAAAAATATACATTTTATCT 727
DB 5981 ATTAAGTTTTTAAAGGAGATTATGAAGATATTTTAAAGTGGGTTATTTTATAGT 6040
QY 728 ATTATAGTTAGCTATTTTTCATGTTAGTAAATATGTTGGAATTGTAATACCTTTT 787
DB 6041 ATGTTTTTGGCCATTAATCGTTTTTGTCTAATCTCTAAACAGATAACGAACGTTTT 6100
QY 788 AAT 790
DB 6101 TAT 6103

RESULT 8
US-08-304-732B-1
Sequence 1, Application US/08304732B
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY
TITLE OF INVENTION: DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY
TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,732B
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1817 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE: Enterococcus faecalis
 US-08-304-732B-1

Query Match 1.4%; Score 26.4; DB 1; Length 1817;
 Best Local Similarity 51.7%; Pred. No. 1.7;
 Matches 60; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
 QY 1306 CATTGATATTTGAACAAATAAATAATGGTAAGTCTCAAGAAATTAGACTATAAGTTA 1365
 DB 618 CAATCGTGAAGAGGAGTTAAATAATTTGTTCTCTGATATCCAGAACTTAAGATC 677
 QY 1366 GAAATATCTTACAGATATAGCAACTATATATATGACCTTCTTAATATGAA 1421
 DB 678 TTGCTTTTATAGTATGCAACGTTAAATAATGAGGCAATATTATTATAA 733

RESULT 9

US-08-304-732B-15
 Sequence 15, Application US/08304732B
 GENERAL INFORMATION:
 APPLICANT: BERGERON, Michel G.
 APPLICANT: OUELLETTE, Marc
 APPLICANT: ROY, Paul H.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY
 TITLE OF INVENTION: DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY
 TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
 TITLE OF INVENTION: LABORATORY
 NUMBER OF SEQUENCES: 134
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Quarles & Brady
 STREET: 411 East Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: USA
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/304,732B
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35,433
 REFERENCE/DOCKET NUMBER: 850586.90012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (414) 277-5591
 TELEFAX: (414) 277-5000
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1348 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Proteus mirabilis
 US-08-304-732B-15

Query Match 1.4%; Score 25.4; DB 1; Length 1348;
 Best Local Similarity 48.9%; Pred. No. 2.7;
 Matches 68; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
 QY 1304 ATCAATCTTGAAGAAATTAATAATGTAAGTCTCAAGAAATTAGACTATAAGT 1363
 DB 13 ATCAATCTTGAAGAAATTAATAATGTAAGTCTCAAGAAATTAGACTATAAGT 72
 QY 1364 TAGAAATATCTTACAGATAAAGCAACTATATATACTAATGACCTTCTTAATATGAAC 1423

Db 73 GAGTTTCAACCAAGCAAAATCATATAGCTTTTAATGTTAGTACCATCTTTATGCTTAC 132
 QY 1424 TGGATATATAAAGTTTCATA 1442
 Db 133 TGCCCGAGAGGAGATAACA 151

RESULT 10

US-08-304-732B-27/c
 Sequence 27, Application US/08304732B
 GENERAL INFORMATION:
 APPLICANT: BERGERON, Michel G.
 APPLICANT: OUELLETTE, Marc
 APPLICANT: ROY, Paul H.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY
 TITLE OF INVENTION: DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY
 TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
 TITLE OF INVENTION: LABORATORY
 NUMBER OF SEQUENCES: 134
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Quarles & Brady
 STREET: 411 East Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: USA
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/304,732B
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35,433
 REFERENCE/DOCKET NUMBER: 850586.90012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (414) 277-5591
 TELEFAX: (414) 277-5000
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9100 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Haemophilus influenzae
 US-08-304-732B-27

Query Match 1.4%; Score 25.4; DB 1; Length 9100;
 Best Local Similarity 49.6%; Pred. No. 2.8;
 Matches 65; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
 QY 560 AATATACCCCTTATCAATCGCTTCTTAAACCTCATCTATATATACATATTTCTCTCC 619
 Db 8079 AATAATACGCTTATCGCGCTTTTTCAGTGTATATATTAAGTCTGTCGACGCCCC 8020
 QY 620 TACTATCTATTCTGTAAGAAGATAAATAACTATGTTTTTTTGTGTTATTTATATAA 679
 Db 8019 ACATCTGAATCTCTCCACACCTAATTTTCGCAACAATTTTGAGATTTCATTGAGTGTAG 7960
 QY 680 AATTATTATA 690
 Db 7959 AACCAAGTAGTA 7949

RESULT 11

US-08-304-732B-26

REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2275 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecalis
US-08-304-732B-2

Query Match 1.3%; Score 23.2; DB 1; Length 2275;
Best Local Similarity 46.8%; Pred. No. 7.3;
Matches 73; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 450 TCTTCCACTCTCTACCGTCAACTTCATCTCTCACTTTTTCGTGTGTACACA 509
DB 1339 TCATTATGTTTGTATGACATCCGATCCGATCAGAAACCAATCCAT 1280
QY 510 TAATCAATATCTTCGTTTACGACTATCGTACTGTGTCACCTAAATATACCCC 569
DB 1279 TGTTCAGTAAGCTGGGTTTTTCAATATATGCGCACTTCTCTGCTAAAGGTTGAA 1220
QY 570 TTATCAATCGCTCTTTAAACTCATCTATATATAC 605
DB 1219 CCACCAATCATATTTTCAAGCGATATATCCAGC 1184

RESULT 14

US-08-304-732B-1/c
Sequence 1, Application US/08304732B
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY
TITLE OF INVENTION: DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY
TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
TITLE OF INVENTION: LABORATORY
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,732B
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1817 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecalis
US-08-304-732B-1
Query Match 1.2%; Score 22.6; DB 1; Length 1817;
Best Local Similarity 45.7%; Pred. No. 9.5;
Matches 79; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
QY 1009 CTCAGAGAAATGCAATCTGTTGATCAACTTTATCTCACCATTATATATATATGTTT 1068
DB 1102 CCTCGATCATCAATACTGTGTGGAATGATCTTCATATATGTTTTCACAAATTT 1043
QY 1069 CAGGCGCAATATGATAAATTAAGAACTGAACCTTAAGAACCAAGAGATGGCACTTTAT 1128
DB 1042 TCCATGCGTATAGGCGTCAATAGCAATCTTGATTAATGTCGTAGTGGCGCTTGAAT 983
QY 1129 TTAAGGATAAAAGCGTTGATATTTATGTTGATAGAAATATTACCATCTCTGTTAT 1181
DB 982 AATAGATAATATTTTGGCATCACTACTGTCATGTAACCCCTGTTAT 930

RESULT 15

US-08-304-732B-26/c
Sequence 26, Application US/08304732B
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY
TITLE OF INVENTION: DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY
TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
TITLE OF INVENTION: LABORATORY
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,732B
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1598 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Haemophilus influenzae
US-08-304-732B-26

Query Match 1.2%; Score 22.4; DB 1; Length 1598;
Best Local Similarity 52.1%; Pred. No. 10;
Matches 50; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy	562	TATACCCCTTATCAATCGCTTCTTTAAACTCATCTATATATATACATATTTGATCCTCCTA	621
Db	371	TATTCCTTTTCATTCCTCAATCTGATTTGTTATTTATCTGAGCATAGAAGTTACATCACCATT	312
Qy	622	CCTATCTATTTCGTAAAGAGATAAAATAAATACTATTGT	657
Db	311	CATATTAAATTTCTAGAAATCAATATATAACGCCACCTGT	276

Search completed: May 11, 2004, 16:57:10
Job time : 60 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 3, 2004, 17:12:26 ; Search time 373 Seconds
(without alignments)
7551.087 Million cell updates/sec

Title: US-10-625-221-12_COPY_918_1580
Perfect score: 663
Sequence: 1 caacaagaccgctccaag.....aagctaccttaacaacccaag 663

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N Geneseq_29Jan04.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002s.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	663	100.0	1851	2	AAT51716
2	663	100.0	1851	2	AAV41593
3	661.4	99.8	756	4	AAH01002
4	661.4	99.8	1837	2	AAT28540
5	661.4	99.8	1837	4	ABA76857
6	658.2	99.3	1837	3	AAZ51112
7	658.2	99.3	1837	6	ABN84229
8	658.2	99.3	1837	7	ACA61184
9	658.2	99.3	1837	8	AAD56771
10	656.6	99.0	1837	8	ACD28901
11	651.8	98.3	1419	8	ACD28908
12	651.8	98.3	1419	8	AAD56778
13	582.6	87.9	1031	7	ACA64700
14	187.4	25.2	1095	7	ACA64696
15	166.8	25.2	773	2	AAT45698
16	166.8	25.2	801	7	ACA64688
17	166.8	25.2	886	7	ACA64689
18	166.8	25.2	1712	3	AAZ51107
19	166.8	25.2	1712	6	ABN84224
20	166.8	25.2	1712	7	ACA61179
21	166.8	25.2	1712	7	ACA64695
22	166.8	25.2	1712	8	ACD28896
23	166.8	25.2	1712	8	AAD56766

24	164.2	24.8	1095	3	AAZ51111
25	164.2	24.8	1095	6	ABN84228
26	164.2	24.8	1095	7	ACA61183
27	164.2	24.8	1095	8	ACD28900
28	164.2	24.8	1095	8	AAZ56770
29	159.2	24.0	867	4	AAH74983
30	158.8	24.0	723	3	AAZ45835
31	158.8	24.0	801	3	AAZ45834
32	158.8	24.0	1388	3	AAZ51109
33	158.8	24.0	1388	6	ABN84226
34	158.8	24.0	1388	7	ACA61181
35	158.8	24.0	1388	8	ACD28898
36	158.8	24.0	1388	8	AAZ56768
37	158.8	24.0	1712	3	AAZ51108
38	158.8	24.0	1712	6	ABN84225
39	158.8	24.0	1712	7	ACA61180
40	158.8	24.0	1712	8	ACD28897
41	158.8	24.0	1712	8	AAZ56767
42	112	16.9	815	3	AAA09240
43	96.6	14.6	1136	7	ACA64697
44	79	11.9	1443	7	ACA64694
45	77.4	11.7	774	9	ADD44369

ALIGNMENTS

RESULT 1
AAT51716
ID AAT51716 standard; DNA; 1851 BP.
AC AAT51716;
XX
DT 04-NOV-1997 (first entry)
XX
DE Streptococcus pyogenes Streptococcal toxin A DNA.
XX
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW hypotension; group A streptococcal infection; myositis; fasciitis;
KW liver damage; T cell; lymphoma; ovarian; uterine; ss.
XX
OS Streptococcus pyogenes.
XX
Key Location/Qualifiers
CDS 828..1583
FT /*tag= a
FT sig_peptide 828..917
FT /*tag= b
FT mat_peptide 918..1580
FT /*tag= c
FT /product= "Streptococcal_toxin_A"
XX
WO9640930-A1.
XX
PD 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US010252.
XX
XX 07-JUN-1995; 95US-00480261.
XX (MINU) UNIV MINNESOTA.
XX Schlievert EM, Roggiani M, Stoehr J, Ohlendorf D;
XX WPI; 1997-099936/09.
XX P-PSDB; AAW12097.
XX
XX Mutant SPE-A toxin with at least one amino acid change is substantially
XX non-lethal - used in vaccine composition for treatment of cancer and
XX streptococcal toxic shock syndrome etc.

PS Disclosure; Page 77-79; 102pp; English.

XX The present sequence encodes Streptococcus pyogenes Streptococcal toxin A
CC (SPE-A), from which a non-lethal mutant SPE-A, comprising at least 1
CC amino acid change, can be derived. The mutant SPE-A can be used to
CC produce vaccines to protect animals against wild type SPE-A and to treat
CC cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A
CC causes neutralising antibodies (Ab) to be produced, which may be used to
CC ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal
CC infection, myositis, fasciitis and liver damage. The neutralising Ab is
CC preferably administered in conjunction with antibiotic therapy. The
CC mutant SPE-A is especially useful for treating T cell lymphomas, and
CC ovarian and uterine cancer. It is thought that mutant SPE-A can be
CC selectively toxic to T cell lymphoma cells

SX Sequence 1851 BP; 635 A; 326 C; 248 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 663; DB 2; Length 1851;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACAAGACCCCGATCCCAAGCCAACTTCACAGATCTAGTTTAAAGACCTTCAAAAT 60
Db |||||
QY 918 CAACAAGACCCCGATCCCAAGCCAACTTCACAGATCTAGTTTAAAGACCTTCAAAAT 977
Db |||||

QY 61 ATATATTTCTTTATGAGGGTGACCTGTTTCTCAGAGAACTGTAATCTGTTGATCAA 120
Db |||||

QY 978 ATATATTTCTTTATGAGGGTGACCTGTTTCTCAGAGAACTGTAATCTGTTGATCAA 1037
Db |||||

QY 121 CTTTATCTCACCATTATATATATATGTTTCAGGCCAAATATGATAAATTAAGAACT 180
Db |||||

QY 1038 CTTTATCTCACCATTATATATATATGTTTCAGGCCAAATATGATAAATTAAGAACT 1097
Db |||||

QY 181 GAACCTTAAGAACCAAGAGATGGCACTTTATTTAAGGATAAAGCTTGTATTTATGTT 240
Db |||||

QY 1098 GAACCTTAAGAACCAAGAGATGGCACTTTATTTAAGGATAAAGCTTGTATTTATGTT 1157
Db |||||

QY 241 GTAGATATTTACCATCTCTGTTTATTTATGTAAGAACTGCAAGAGGATGCTATCTAC 300
Db |||||

QY 1158 GTAGATATTTACCATCTCTGTTTATTTATGTAAGAACTGCAAGAGGATGCTATCTAC 1217
Db |||||

QY 301 GGAGGGGTAAACAAATCATGAAGGGAATCAATTTAGAAATTCCTAAAGAGATAGTCGTTAAA 360
Db |||||

QY 1218 GGAGGGGTAAACAAATCATGAAGGGAATCAATTTAGAAATTCCTAAAGAGATAGTCGTTAAA 1277
Db |||||

QY 361 GTATCATCGATGGTATCCAAAGCCATCATTTGATGTAACAAATTAAGAAATGGTA 420
Db |||||

QY 1278 GTATCATCGATGGTATCCAAAGCCATCATTTGATGTAACAAATTAAGAAATGGTA 1337
Db |||||

QY 421 ACTGCTCAAGATTTAGACTATAAAGTTAGAAATATCTTACAGATATAAGCAACTATAT 480
Db |||||

QY 1338 ACTGCTCAAGATTTAGACTATAAAGTTAGAAATATCTTACAGATATAAGCAACTATAT 1397
Db |||||

QY 481 ACTAATGGACCTTTAAATATGAACCTGGATATATAAGTTTCATCTAAGATAAAGAA 540
Db |||||

QY 1398 ACTAATGGACCTTTAAATATGAACCTGGATATATAAGTTTCATCTAAGATAAAGAA 1457
Db |||||

QY 541 AGTTTTTGGTTGATTTTTCCTGACCAAGCAATTTACTCAATCTAAATATCTTATGATA 600
Db |||||

QY 1458 AGTTTTTGGTTGATTTTTCCTGACCAAGCAATTTACTCAATCTAAATATCTTATGATA 1517
Db |||||

QY 601 TATAAGATATAAGAAAGCTTGAATCAACACAGCAAGCAATTTGAAGTCTACCTAAGAAC 660
Db |||||

QY 1518 TATAAGATATAAGAAAGCTTGAATCAACACAGCAAGCAATTTGAAGTCTACCTAAGAAC 1577
Db |||||

QY 661 AAG 663
Db |||||

QY 1578 AAG 1580

RESULT 2
AAV41593
ID

AAV41593 standard; DNA; 1851 BP.

XX AAV41593;

XX 12-OCT-1998 (first entry)

XX Nucleotide sequence of Streptococcus pyogenes exotoxin A.

XX SPE-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin A;
XX wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer;
XX streptococcal toxic shock syndrome; STSS; T cell lymphoma;
XX uterine cancer; ss.

XX Streptococcus pyogenes.

XX Key Location/Qualifiers
XX CDS 828..1583

XX /*tag= a
XX /product= "SPE-A toxin"

XX WO9824911-A2.

XX 11-JUN-1998.

XX 05-DEC-1997; 97WO-US022228.

XX 06-DEC-1996; 96US-0032930P.

XX (MINU) UNIV MINNESOTA.

XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;

XX WPI; 1998-333330/29.

XX P-PSDB; AAW59780.

XX New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention or
XX treatment of streptococcal infection or toxic shock syndrome.

XX Disclosure; Fig 3; 95pp; English.

XX This is the nucleotide sequence of the Streptococcus pyogenes exotoxin A
CC (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin has at least 1
CC aa change and is nonlethal compared with a protein to wild type SPE-A
CC toxin. The mutant SPE-A toxins are nontoxic and can produce antibodies
CC that neutralise wild type SPE-A toxin activity. The toxins can be used in
CC vaccines and therapeutics to generate a protective immune response
CC against streptococcal infection. They can be used to protect against the
CC development of streptococcal toxic shock syndrome (STSS). In addition,
CC the toxins can be used for treating animals with symptoms of
CC streptococcal infection or STSS and in methods for stimulating T cell
CC proliferation and in the treatment of cancer. In particular they can be
CC used for treating T cell lymphomas, and ovarian and uterine cancer

XX Sequence 1851 BP; 635 A; 326 C; 248 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 663; DB 2; Length 1851;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACAAGACCCCGATCCCAAGCCAACTTCACAGATCTAGTTTAAAGACCTTCAAAAT 60
Db |||||

QY 918 CAACAAGACCCCGATCCCAAGCCAACTTCACAGATCTAGTTTAAAGACCTTCAAAAT 977
Db |||||

QY 61 ATATATTTCTTTATGAGGGTGACCTGTTTCTCAGAGAACTGTAATCTGTTGATCAA 120
Db |||||

QY 978 ATATATTTCTTTATGAGGGTGACCTGTTTCTCAGAGAACTGTAATCTGTTGATCAA 1037
Db |||||

QY 121 CTTTATCTCACCATTATATATATATGTTTCAGGCCAAATATGATAAATTAAGAACT 180
Db |||||

QY 1038 CTTTATCTCACCATTATATATATATGTTTCAGGCCAAATATGATAAATTAAGAACT 1097
Db |||||

QY 181 GAACCTTAAGAACCAAGAGATGGCACTTTATTTAAGGATAAAGCTTGTATTTATGTT 240
Db |||||

QY 1098 GAACCTTAAGAACCAAGAGATGGCACTTTATTTAAGGATAAAGCTTGTATTTATGTT 1157
Db |||||

QY 241 GTAGAATATACCATCTCTGTTATTTATGTAATGAGAAAGGAGTCCATGTATCTAC 300
 Db |||||
 QY 1158 GTAGAAATATACCATCTCTGTTATTTATGTAATGAGAAAGGAGTCCATGTATCTAC 1217
 Db |||||
 QY 301 GGAGGGGTAAACAAATCATGAAGGGGAATCATTTAGAAATTCCTTAAAGAGATAGTCGTTAAA 360
 Db |||||
 QY 1218 GGAGGGGTAAACAAATCATGAAGGGGAATCATTTAGAAATTCCTTAAAGAGATAGTCGTTAAA 1277
 Db |||||
 QY 361 GTATCAATCGATGGTATCCAAAGCCCTATCATTTGATATTTGAAACAAATTAAGAAATGGTA 420
 Db |||||
 QY 1278 GTATCAATCGATGGTATCCAAAGCCCTATCATTTGATATTTGAAACAAATTAAGAAATGGTA 1337
 Db |||||
 QY 421 ACTGCTCAAGAAATAGACTATATAAGCTTAGAAATATCTTACAGATAAAGCAACTATAT 480
 Db |||||
 QY 1338 ACTGCTCAAGAAATAGACTATATAAGCTTAGAAATATCTTACAGATAAAGCAACTATAT 1397
 Db |||||
 QY 481 ACTAATGACCTTCTTAATATGAACACTGGATATATAAAGTTTCAATACCTTAAGAAATGAAGAA 540
 Db |||||
 QY 1398 ACTAATGACCTTCTTAATATGAACACTGGATATATAAAGTTTCAATACCTTAAGAAATGAAGAA 1457
 Db |||||
 QY 541 AGTTTGTGGTTGATTTTCCCTGACCAACAGAAATTTACTCAATCTAAATATCTTATGATA 600
 Db |||||
 QY 1458 AGTTTGTGGTTGATTTTCCCTGACCAACAGAAATTTACTCAATCTAAATATCTTATGATA 1517
 Db |||||
 QY 601 TATAAGATAATGAACGCTTGACTCAACCAAGCCAAATTTGAAGTCTACTTAACRACC 660
 Db |||||
 QY 1518 TATAAGATAATGAACGCTTGACTCAACCAAGCCAAATTTGAAGTCTACTTAACRACC 1577
 Db |||||
 QY 661 AAG 663
 Db |||||
 QY 1578 AAG 1580

RESULT 3

AAH01002
 ID AAH01002 standard; DNA; 756 BP.
 XX
 AC AAH01002;
 XX
 DT 24-JUL-2001 (first entry)
 XX
 DE Unidentified nucleotide sequence SEQ ID NO:993.
 XX
 KW Species specific; genus specific; family specific; probe; detection;
 KW identification; algal; archaeal; bacterial; fungal; parasitological;
 KW microorganism; diagnosis; translation elongation factor Tu; toxin;
 KW translation elongation factor G; RecA recombinase; resistance;
 KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 KW primer; ds.
 XX

Unidentified.

XX
 PN WO200123604-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000WO-CAP01150.
 XX
 PR 28-SEP-1999; 99CA-02283458.
 PR 19-MAY-2000; 2000CA-02307010.
 XX

(INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

XX
 PA Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
 PI Picard FJ, Roy PH;
 XX
 DR WPI; 2001-245006/25.
 XX

XX
 PT Nucleic acid sequences are used to generate universal probes and primers
 PT which can be used to identify and detect the presence of algal, archaeal,
 PT bacterial, fungal and parasitological species in a test sample.
 XX

PS Disclosure; Page 957; 1580pp; English.

XX The present invention describes a method for generating a repository of
 CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
 CC and/or primers are derived. The method comprises amplifying the nucleic
 CC acids of determined algal, archaeal, bacterial, fungal and parasitological
 CC species with a combination of defined primer pairs. The method can be
 CC used for producing probes and/or primers for detecting one or more
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 CC parasites, for universal detection and for specific and ubiquitous
 CC detection and identification of an algal, archaeal, bacterial, fungal and
 CC parasitological species, genus, family and group. A nucleic acid (I) obtained
 CC using the method of the invention can be used for the universal detection
 CC of any bacterium, fungus or parasite in a sample and for the detection of
 CC at least one antimicrobial agent resistance gene or at least one toxin
 CC gene. hexA nucleic acids are used for the specific and ubiquitous
 CC detection and for identification of Streptococcus pneumoniae. (I) can be
 CC used to design a therapeutic agent which is effective against
 CC microorganisms. Microbial species or genus or family or phylum or group
 CC which can be detected include Abiotrophia adiacens, Escherichia coli,
 CC Corynebacterium sp., Enterobacteriaceae group, Streptococcus sp., Neisseria
 CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
 CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
 CC results than substrate specificity tests as results can be determined in
 CC an hour and improved accuracy is also achieved. AAH00010 to AAH002104
 CC represent nucleotide sequences and primers/probes which are given in the
 CC exemplification of the present invention
 XX

Sequence 756 BP; 297 A; 110 C; 118 G; 231 T; 0 U; 0 Other;

Query Match 99.8%; Score 561.4; DB 4; Length 756;

Best Local Similarity 99.8%; Pred. No. 2e-120;

Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAACAAGACCCCGATCCAAAGCCAACTTCACAGATCTAGTTTAGTAAACCTTCACAAAT 60
 Db |||||
 QY 91 CAACAAGACCCCGATCCAAAGCCAACTTCACAGATCTAGTTTAGTAAACCTTCACAAAT 150
 Db |||||
 QY 61 ATATATTTTCTTTATGAGGGTGACCTGTACTCACGAGAAATGTGAATCTGTGTGACAA 120
 Db |||||
 QY 151 ATATATTTTCTTTATGAGGGTGACCTGTACTCACGAGAAATGTGAATCTGTGTGACAA 210
 Db |||||
 QY 121 CTTTATCTCACCATTAAATATATATATGTTTCAGGCGCAATATGATAAATTAATAACT 180
 Db |||||
 QY 211 CTTTATCTCACCATTAAATATATATATGTTTCAGGCGCAATATGATAAATTAATAACT 270
 Db |||||
 QY 181 GAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGCATTAACGTTGATATTATGGT 240
 Db |||||
 QY 271 GAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATTAACGTTGATATTATGGT 330
 Db |||||
 QY 241 GTAGAATATTACCATCTCTGTTATTTATGTGAAATGCAGAAAGGAGTGCATGTATCTAC 300
 Db |||||
 QY 331 GTAGAATATTACCATCTCTGTTATTTATGTGAAATGCAGAAAGGAGTGCATGTATCTAC 390
 Db |||||
 QY 301 GGAGGGGTACAAATCATGAGGGAATCATTTAGAAATTCCTTAAAGATAGTCGTTAAA 360
 Db |||||
 QY 391 GGAGGGGTACAAATCATGAGGGAATCATTTAGAAATTCCTTAAAGATAGTCGTTAAA 450
 Db |||||
 QY 361 GTATCAATCGATGGTATCCAAAGCCCTATCATTTGATATTGAAACAAATTAAGAAATGGTA 420
 Db |||||
 QY 451 GTATCAATCGATGGTATCCAAAGCCCTATCATTTGATATTGAAACAAATTAAGAAATGGTA 510
 Db |||||
 QY 421 ACTGCTCAAGAAATAGACTATATAAAGTTAGAAATATCTTTACAGATAAAGCAACTATAT 480
 Db |||||
 QY 511 ACTGCTCAAGAAATAGACTATATAAAGTTAGAAATATCTTTACAGATAAAGCAACTATAT 570
 Db |||||
 QY 481 ACTAATGACCTTCTTAATATGAACACTGGATATATAAAGTTTCAATACCTTAAGAAATGAAGAA 540
 Db |||||
 QY 571 ACTAATGACCTTCTTAATATGAACACTGGATATATAAAGTTTCAATACCTTAAGAAATGAAGAA 630
 Db |||||
 QY 541 AGTTTGTGGTTGATTTTCCCTGACCAACAGAAATTTACTCAATCTAAATATCTTATGATA 600
 Db |||||
 QY 631 AGTTTGTGGTTGATTTTCCCTGACCAACAGAAATTTACTCAATCTAAATATCTTATGATA 690
 Db |||||

29-JUN-2001.
 12-SEP-1995; 95NZ-00501596.
 12-SEP-1995; 95NZ-00501596.
 (JDII-) IDI INFECTIO DIAGNOSTIC INC.
 Bergeron MG, Ouellette M, Roy PH;
 WPI; 2001-615034/71.
 Method for detecting target bacterial species in a sample, comprises detecting the presence or amount of bacterial nucleic acid amplified by a primer derived from bacterial DNA, specific for the target bacterial species.
 Claim 6; Page 107-108; 168pp; English.
 The invention relates to detecting target bacterial species suspected to be present in a sample, comprising contacting nucleic acids of target bacterial species with an amplification primer pair derived from a bacterial DNA fragment (ABA76825-ABA76861) specific for the target bacterial species but ubiquitous for different strains, amplifying the nucleic acid and detecting the presence or amount of an amplified sequence as an indication of the presence or amount of the target bacterial species. The invention includes primers and probes (ABA76862-ABA76984) against the target bacterial species, especially E.coli, K.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae, S.aureus, S.epidermidis, E.faecalis, S.saprophyticus, S.pyogenes, H.influenzae, M.catarrhalis and/or group A Streptococcus producing exotoxin A gene spe A, suspected to be present in a sample which is obtained from human patients, animals, environment or food, and which consists of one or more bacterial colonies. Oligonucleotide probes and primers complementary to the bacterial genes encoding resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aadC1, aacC2, aacC3, aacA4, mecA, vanA, vanH, vanX, satA, aac-aphD, vat, yga, msrA, sul and/or int (ABA76985-ABA77001) are also useful to identify commonly encountered and clinically important resistance genes. The invention provides a rapid method of bacterial identification that can be achieved, which reduces the time currently required for the identification of pathogens in the clinical laboratory
 SQ Sequence 1837 BP; 631 A; 318 C; 248 G; 640 T; 0 U; 0 Other;

Query Match 99.8%; Score 661.4; DB 4; Length 1837;
 Best local Similarity 99.8%; Pred. No. 2.1e-120;
 Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 CAACAAGACCCGATCCAGCCAACTTCACAGATCTAGTTAGTAAACCTTCAAAT 60
 904 CAACAAGACCCGATCCAGCCAACTTCACAGATCTAGTTAGTAAACCTTCAAAT 963
 61 ATATATTTCTTTATGAGGTGACCCCTGTACTCACGAGAAATGTGAATCTGTGTACAA 120
 964 ATATATTTCTTTATGAGGTGACCCCTGTACTCACGAGAAATGTGAATCTGTGTACAA 1023
 121 CTTTATCTCACCATTAAATATAATGTTTCAGGCGCAATTAATGATAAATTAATAACT 180
 1024 CTTTATCTCAGGATTAATATAATGTTTCAGGCGCAATTAATGATAAATTAATAACT 1083
 181 GAATTAAGACCCAGAGATGCGCACTTATTAAGATAAATTAATGATAAATTAATAACT 240
 1084 GAATTAAGACCCAGAGATGCGCACTTATTAAGATAAATTAATGATAAATTAATAACT 1143
 241 GTAGATATTACCACTCTCTGTTATTTATGTAATATGCAAAATGCAAGAGTGCATGTCTAC 300
 1144 GTAGATATTACCACTCTCTGTTATTTATGTAATATGCAAAATGCAAGAGTGCATGTCTAC 1203
 301 GGAGGGGTACAAATCATGAGGGAATCATTTAGAAATTCCTAAAGAGATGTCGTTAAA 360
 1204 GGAGGGGTACAAATCATGAGGGAATCATTTAGAAATTCCTAAAGAGATGTCGTTAAA 1263

QY 361 GTATCAATCGATCGTATCCAAAGCCTATCATTTGATATTTGAAACAAATATAAAAAATGGTA 420
 DB 1264 GTATCAATCGATCGTATCCAAAGCCTATCATTTGATATTTGAAACAAATATAAAAAATGGTA 1323
 QY 421 ACTGCTCAAGAAATAGACTATATAAGTTAGAAAATATCTTACAGATATAAAGCAACTATAT 480
 DB 1324 ACTGCTCAAGAAATAGACTATATAAGTTAGAAAATATCTTACAGATATAAAGCAACTATAT 1383
 QY 481 ACTAATGCACTTCTAAATATGAAACTGGATATATAAAGTTCACTACCTAAGATAAGAA 540
 DB 1384 ACTAATGCACTTCTAAATATGAAACTGGATATATAAAGTTCACTACCTAAGATAAGAA 1443
 QY 541 AGTTTTTGGTTGATTTTTTCCCTGACCAAGCAATTTACTCAATCTAATATCTTATGATA 600
 DB 1444 AGTTTTTGGTTGATTTTTTCCCTGACCAAGCAATTTACTCAATCTAATATCTTATGATA 1503
 QY 601 TATAAAGATAATGAAACGCTTGACTCAACACAGCCAAATTTGAAGTCTACTAACCAAC 660
 DB 1504 TATAAAGATAATGAAACGCTTGACTCAACACAGCCAAATTTGAAGTCTACTAACCAAC 1563
 QY 661 AAG 663
 DB 1564 AAG 1566

RESULT 6

AZ51112
 ID AZ51112 standard; DNA; 1837 BP.

AC AZ51112;
 XX

DT 05-JUN-2000 (first entry)
 XX

XX Streptococcal pyrogenic exotoxin A (SPE-A) encoding DNA.

XX Superantigen toxin; SAg; Streptococcal pyrogenic exotoxin A; SPE-A;
 XX antibacterial; vaccine; WBC class II receptor; T-cell antigen receptor;
 XX cytosolic; antibody; staphylococcal/streptococcal toxin; toxoid; SPEA42;
 XX diagnosis; treatment; superantigen-associated bacterial infection; ds.
 XX

OS Streptococcus sp.

PH Key Location/Qualifiers
 FT CDS 814..1569

FT tag= a
 XX /product= "Streptococcal pyrogenic exotoxin A (SPE-A)"

XX WO200009154-A1.
 XX

PD 24-FEB-2000.
 XX

XX 13-AUG-1998; 98WO-US016766.
 XX

XX 13-AUG-1998; 98WO-US016766.
 XX

XX (REED-) REED ARMY INST RES WALTER.
 XX

XX Ulrich RG, Olson MA, Bavari S;
 XX

XX WPI; 2000-224177/19.
 XX

XX P-PSDB; AAY70109.
 XX

XX Nucleic acid encoding superantigen toxin useful as a vaccine and for
 PT diagnosis of superantigen-associated bacterial infections.
 XX

XX Example 12; Page 92-94; 118pp; English.
 XX

XX The present sequence is the DNA encoding Streptococcal pyrogenic exotoxin
 CC A (SPE-A), a bacterial superantigen toxin (SAG), used for the formulation
 CC of SPE-A vaccine SPEA42. The coding region of this SAG toxin is altered
 CC by site directed mutagenesis, introducing L42R mutation, that results in
 CC disruption of binding of the toxin to both the MHC class II or T-cell
 CC antigen receptor. SPE-A has antibacterial and cytostatic activity. This

sequence is useful for the production of SPE-A vaccines and specific antibodies. This vaccine overcomes the disadvantages of the chemically inactivated toxoids and is designed to protect individuals against one or several related staphylococcal and streptococcal toxins. It is used for the diagnosis and treatment or amelioration of superantigen-associated bacterial infections

Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;

Query Match 99.3%; Score 658.2; DB 3; Length 1837;
Best Local Similarity 99.5%; Pred. No. 8.8e-120;
Matches 660; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACAAGACCCCGATCCCAAGCAACTTCACAGATCTAGTTTGTATTAAGAACTTCAAAAT 60
DB 904 CAACAAGACCCCGATCCCAAGCAACTTCACAGATCTAGTTTGTATTAAGAACTTCAAAAT 963

QY 61 ATATATTTTCTTTATGAGGGTGACCTGTTACTACGAGAAATGCGAAATCTGTGATCAA 120
DB 964 ATATATTTTCTTTATGAGGGTGACCTGTTACTACGAGAAATGCGAAATCTGTGATCAA 1023

QY 121 CTTTATCTCACCATTATATATATATATGTTTCAGGGCCAAATATGATAAATTAAGAACT 180
DB 1024 CTTAGATCTCAGATTATATATATATGTTTCAGGGCCAAATATGATAAATTAAGAACT 1083

QY 181 GAACTTAAGAACCAAGAGATGCGAACTTTATTTAAGGATAAAGCTGTGATTTATGTT 240
DB 1084 GAACTTAAGAACCAAGAGATGCGAACTTTATTTAAGGATAAAGCTGTGATTTATGTT 1143

QY 241 GTAGAAATATACCATCTCTGTTTATTTATGTAAGAAATGAGAAAGGAGTGCATGTATC 300
DB 1144 GTAGAAATATACCATCTCTGTTTATTTATGTAAGAAATGAGAAAGGAGTGCATGTATC 1203

QY 301 GGAGGGGTAAACAAATCAAGAGGAACTATTTAGAAATTCCTTAAAGAGATAGTCTGTTAA 360
DB 1204 GGAGGGGTAAACAAATCAAGAGGAACTATTTAGAAATTCCTTAAAGAGATAGTCTGTTAA 1263

QY 361 GTATCAATCGATGGTATCCAAAGCTATCATTTGATATTTGAACAAATAAAGAAATGGTA 420
DB 1264 GTATCAATCGATGGTATCCAAAGCTATCATTTGATATTTGAACAAATAAAGAAATGGTA 1323

QY 421 ACTGCTCAAGAAATTAGACTATTAAGTTAGAAATATCTTTACAGATAATAAGCAACTATAT 480
DB 1324 ACTGCTCAAGAAATTAGACTATTAAGTTAGAAATATCTTTACAGATAATAAGCAACTATAT 1383

QY 481 ACTAATGGACCTTCTAATATCAAACTGGATATATAAGTTTCATACCTTAAGAAATAAGAA 540
DB 1384 ACTAATGGACCTTCTAATATCAAACTGGATATATAAGTTTCATACCTTAAGAAATAAGAA 1443

QY 541 AGTTTTTGGTTTGAATTTTCCCTGAACCAAGAAATTTACTCAATCTAAATATCTTATGATA 600
DB 1444 AGTTTTTGGTTTGAATTTTCCCTGAACCAAGAAATTTACTCAATCTAAATATCTTATGATA 1503

QY 601 TATAAGATAATGAACCGCTTGACTCAACACAAAGCCAAATTTGAAGTCTTACCTAACCAACC 660
DB 1504 TATAAGATAATGAACCGCTTGACTCAACACAAAGCCAAATTTGAAGTCTTACCTAACCAACC 1563

QY 661 AAG 663
DB 1564 AAG 1566

RESULT 7

ABN84229
ID ABN84229 standard; cDNA; 1837 BP.
XX AC ABN84229;
XX DT 23-SEP-2002 (first entry)
XX DE Streptococcal pyrogenic exotoxin A vaccine SPEa42 coding sequence.
XX EX Exotoxin A; SPEa; SPEa42; superantigen; antigen; toxin; vaccine;

KW attenuation; mutant; gene; ss.
XX Streptococcus pyogenes.
OS Synthetic.

Key Location/Qualifiers
FT 814..1569
CDS /*tag= a
/product= "SPEa42"

US6399332-B1.

04-JUN-2002.

01-SEP-1998; 98US-00144776.

25-JUN-1997; 97US-00882431.

(USSA) US SEC OF ARMY.

Ulrich RG, Olson MA, Bavari S;

WPI; 2002-546281/58.

P-PSDB; 98B79508.

Novel isolated and purified superantigen toxin DNA fragment which has been genetically altered, useful for producing vaccine for treatment of superantigen toxin-associated bacterial diseases.

Disclosure; Col 61-63; 46pp; English.

The present sequence is the coding sequence of Streptococcus pyogenes vaccine SPEa42. The vaccine differs from the native SPEa sequence by substitution of the Leu-42 residue by Arg. This mutation is expected to disrupt contact between the toxin and the HLA-DR receptor, reducing DRI binding. SPEa42 can be expressed as a recombinant protein in Escherichia coli as a secreted protein or as a cytoplasmic product. No indicators of toxicity have been detected for the purified recombinant protein, and vaccine studies demonstrate that SPEa42 is highly antigenic, inducing protective immunity in a mouse animal model. The attenuated superantigen can be used to protect against superantigen toxin infections. Methods of producing and using altered superantigen toxins as vaccines, and in diagnosis and therapy, are provided by the invention. A multivalent vaccine consisting of altered superantigen toxins from SEA, SEB, SEC-1, TSSP-1 and SPEa is predicted to provide protective immunity against the majority of bacterial superantigen toxins

Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;

Query Match 99.3%; Score 658.2; DB 6; Length 1837;
Best Local Similarity 99.5%; Pred. No. 8.8e-120;
Matches 660; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACAAGACCCCGATCCCAAGCAACTTCACAGATCTAGTTTGTATTAAGAACTTCAAAAT 60
DB 904 CAACAAGACCCCGATCCCAAGCAACTTCACAGATCTAGTTTGTATTAAGAACTTCAAAAT 963

QY 61 ATATATTTTCTTTATGAGGGTGACCTGTTACTACGAGAAATGCGAAATCTGTGATCAA 120
DB 964 ATATATTTTCTTTATGAGGGTGACCTGTTACTACGAGAAATGCGAAATCTGTGATCAA 1023

QY 121 CTTTATCTCACCATTATATATATATGTTTCAGGGCCAAATATGATAAATTAAGAACT 180
DB 1024 CTTAGATCTCAGATTATATATATGTTTCAGGGCCAAATATGATAAATTAAGAACT 1083

QY 181 GAACTTAAGAACCAAGAGATGCGAACTTTATTTAAGGATAAAGCTGTGATTTATGTT 240
DB 1084 GAACTTAAGAACCAAGAGATGCGAACTTTATTTAAGGATAAAGCTGTGATTTATGTT 1143

QY 241 GTAGAAATATACCATCTCTGTTTATTTATGTAAGAAATGAGAAAGGAGTGCATGTATC 300
DB 1144 GTAGAAATATACCATCTCTGTTTATTTATGTAAGAAATGAGAAAGGAGTGCATGTATC 1203

QY 301 GGAGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAA 360
Db 1204 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAA 1263
QY 361 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATAAAAAATGGTA 420
Db 1264 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATAAAAAATGGTA 1323
QY 421 ACTGCTCAAGAAATAGACTATATAAGTTAGAAAATATCTTACAGATAAAGCAACTATAT 480
Db 1324 ACTGCTCAAGAAATAGACTATATAAGTTAGAAAATATCTTACAGATAAAGCAACTATAT 1383
QY 481 ACTAATGACCTCTTAAATATGAACACTGGATATATAAAGTTTCATACCTAAAGATAAGAA 540
Db 1384 ACTAATGACCTCTTAAATATGAACACTGGATATATAAAGTTTCATACCTAAAGATAAGAA 1443
QY 541 AGTTTGGTGTGATTTTCCCTGAACCAAGATTTACTCAATCTAAATATCTTATGATA 600
Db 1444 AGTTTGGTGTGATTTTCCCTGAACCAAGATTTACTCAATCTAAATATCTTATGATA 1503
QY 601 TATAAGATAATGAACCTTTGACTCAACCAAGCCTAAATGAGTCTTACCTAACCAACC 660
Db 1504 TATAAGATAATGAACCTTTGACTCAACCAAGCCTAAATGAGTCTTACCTAACCAACC 1563
QY 661 AAG 663
Db 1564 AAG 1566

RESULT 8

ACA61184
ID ACA61184 standard; DNA; 1837 BP.

AC ACA61184;

11-AUG-2003 (first entry)

DNA encoding streptococcal pyrogenic exotoxin A.

Pyrogenic exotoxin A; ds; superantigen-associated bacterial infection;
superantigen toxin; gene; vaccine.

Streptococcus sp.

Key Location/Qualifiers
CDS 814..1569

/*tag= a
/product= "Pyrogenic exotoxin A"

US2003009015-A1.

09-JAN-2003.

25-JUN-1997; 97US-00882431.

25-JUN-1997; 97US-00882431.

(ULRI/) ULRICH R G.

(OLSO/) OLSON M A.

(BAVA/) BAVARI S.

Ulrich RG, Olson MA, Bavari S;

WPI; 2003-401542/38.

P-PSDB; ABU10088.

New superantigen toxin and/or DNA fragment with an altered binding of the
encoded altered toxin to either MHC class II or T cell antigen receptor,
useful for treating or ameliorating superantigen-associated bacterial
infection.

Claim 9; Page 32-34; 50pp; English.

CC The invention relates to an isolated and purified superantigen toxin
CC and/or DNA fragment, which has been altered so that the binding of the
CC encoded toxin to either major histocompatibility complex (MHC) class II
CC or T cell antigen receptor is altered. The superantigen toxins, DNA
CC fragments, and vaccines are useful for treating or ameliorating
CC superantigen-associated bacterial infection. The DNA fragments are
CC particularly useful for producing vaccine against superantigen toxin
CC infections. The transformed host cells are useful for analysing the
CC effectiveness of drugs and agents that affect the binding of
CC superantigens to MHC class II or T-cell antigen receptors. The present
CC sequence represents DNA encoding streptococcal pyrogenic exotoxin A
XX

SQ Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;

Query Match 99.3%; Score 658.2; DB 7; Length 1837;

Best Local Similarity 99.5%; Pred. No. 8.8-120;

Matches 660; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACAAGACCCCGATCCAAAGCCAACTTCACAGATCTAGTTAGTAAAGACCTTCAAAAT 60

Db 904 CAACAAGACCCCGATCCAAAGCCAACTTCACAGATCTAGTTAGTAAAGACCTTCAAAAT 963

QY 61 ATATATTTCTTTATGAGGGTGACCCCTGTACTCACGAGATGTGAATCTGTTGATCAA 120

Db 964 ATATATTTCTTTATGAGGGTGACCCCTGTACTCACGAGATGTGAATCTGTTGATCAA 1023

QY 121 CTTTATCTCACCATTAAATATATAATGTTTCAGGGCCAAATTAATGATAAATAAACT 180

Db 1024 CTTAGATCTCAGATTTAAATATATAATGTTTCAGGGCCAAATTAATGATAAATAAACT 1083

QY 181 GAACCTTAAGACCAAGAGATGGCACTTTATTAAGGATAAAGACCTTGATTTATGGT 240

Db 1084 GAACCTTAAGACCAAGAGATGGCACTTTATTAAGGATAAAGACCTTGATTTATGGT 1143

QY 241 GTAGATATTTACCATCTCTGTTATTTATGTGAAAATGCAGAAAGAGTGATGATCTAC 300

Db 1144 GTAGATATTTACCATCTCTGTTATTTATGTGAAAATGCAGAAAGAGTGATGATCTAC 1203

QY 301 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAA 360

Db 1204 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAA 1263

QY 361 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATAAAAAATGGTA 420

Db 1264 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATAAAAAATGGTA 1323

QY 421 ACTGCTCAAGAAATTAGACTATATAAGTTAGAAAATATCTTACAGATAAAGCAACTATAT 480

Db 1324 ACTGCTCAAGAAATTAGACTATATAAGTTAGAAAATATCTTACAGATAAAGCAACTATAT 1383

QY 481 ACTAATGGACCTTCTAAATATGAACCTGGATATATAAAGTTCTATACCTAAGATAAGAA 540

Db 1384 ACTAATGGACCTTCTAAATATGAACCTGGATATATAAAGTTCTATACCTAAGATAAGAA 1443

QY 541 AGTTTTTGGTTGATTTTCCCTGACCAAGATTTTACTCAATCTTAATATCTTATGATA 600

Db 1444 AGTTTTTGGTTGATTTTCCCTGACCAAGATTTTACTCAATCTTAATATCTTATGATA 1503

QY 601 TATAAAGATAATGAACCTGTTGACTCAACACAGCCAAATTTGAAGTCTACCTAACCAACC 660

Db 1504 TATAAAGATAATGAACCTGTTGACTCAACACAGCCAAATTTGAAGTCTACCTAACCAACC 1563

QY 661 AAG 663

Db 1564 AAG 1566

RESULT 9

AAD56771

ID AAD56771 standard; DNA; 1837 BP.

XX

AC AAD56771;

XX

06-OCT-2003 (first entry)

Streptococcus pyogenes pyrogenic exotoxin A (SpeA) DNA.

Superantigen toxin; vaccine; infection; pyrogenic exotoxin A; SpeA; gene therapy; gene; ds.

Streptococcus pyogenes.

Key: Location/Qualifiers
CDS 814..1566
/tag= a
/product= "Streptococcus pyogenes SpeA protein"
/transl_except= (pos:901..903, aa:Met)
/note= "This translational exception occurs only when decoding SEQ ID NO: 26 (AAE37687)"

sig_peptide 814..900
/tag= b

mat_peptide 901..1566
/tag= c
/product= "Streptococcus pyogenes mature SpeA protein"

WO2003056015-A1.

10-JUL-2003.

26-NOV-2001; 2001WO-US046540.

26-NOV-2001; 2001US-00002784.

(USME-) US MEDICAL RES INST INFECTIOUS DISEASES.

Ulrich RG;

WPI; 2003-492125/46.

P-PSDB; AAE37683, AAE37687

New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.

Claim 4; Page 128-129; 141pp; English.

The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes pyrogenic exotoxin A (SpeA) DNA. This sequence is used in the invention

Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;

Query Match 99.3%; Score 658.2; DB 8; Length 1837;
Best Local Similarity 99.5%; Pred. No. 8.e-120;
Matches 660; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CAACAGACCCGATCCAGCCCACTTCACAGATCTAGTTAGTAAACCTTCAAAAT 60
904 CAACAGACCCGATCCAGCCCACTTCACAGATCTAGTTAGTAAACCTTCAAAAT 963

61 ATATATTTTCTTATGAGGTCACCTGTCTACAGAGATGTGAAATCTGTGATCAA 120
964 ATATATTTTCTTATGAGGTCACCTGTCTACAGAGATGTGAAATCTGTGATCAA 1023

121 CTTTATCTCACCATTATATATATATATATATATATATATATATATATATATAT 180
1024 CTTATATCTCAGATTATATATATATATATATATATATATATATATATATATAT 1083

181 GAACCTTAAGAACCAAGAGATGCACTTTATTTTAAAGNTAAACCTGTATATGTT 240
1084 GAACCTTAAGAACCAAGAGATGCACTTTATTTTAAAGNTAAACCTGTATATGTT 1143

241 GTAGAATATTACCATCTCTGTTATTTATTTATGTAATATSCAGAAAGGAGTGTATCTAC 300

Db 1144 GTAGAATATTACCATCTCTGTTATTTATTTATGTAATATSCAGAAAGGAGTGTATCTAC 1203

Qy 301 GGAGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCTGTTAAA 360

Db 1204 GGAGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCTGTTAAA 1263

Qy 361 GTATCAATCGATGGTATCCAAAGCCTCATCTTGTATTTGAAACAAATATAAAAAATGGTA 420

Db 1264 GTATCAATCGATGGTATCCAAAGCCTCATCTTGTATTTGAAACAAATATAAAAAATGGTA 1323

Qy 421 ACTGCTCAAGAAATTAGACTATAAAGTTAGAAATATCTTACAGATAATAAGCAACTATAT 480

Db 1324 ACTGCTCAAGAAATTAGACTATAAAGTTAGAAATATCTTACAGATAATAAGCAACTATAT 1383

Qy 481 ACTAATGACCTCTTAATATAGAACTGGATATATAAGTTTCACTACCTTAAGNATAAGAA 540

Db 1384 ACTAATGACCTCTTAATATAGAACTGGATATATAAGTTTCACTACCTTAAGNATAAGAA 1443

Qy 541 AGTTTTTGGTTTGAATTTTCCCTGAACAGAAATTTACTCAATCTAAATATCTTATGATA 600

Db 1444 AGTTTTTGGTTTGAATTTTCCCTGAACAGAAATTTACTCAATCTAAATATCTTATGATA 1503

Qy 601 TATAAGATAATGAACCGCTTGACTCAACACCAAGCCAAATTTGAAGTCTTACCTAAACACC 660

Db 1504 TATAAGATAATGAACCGCTTGACTCAACACCAAGCCAAATTTGAAGTCTTACCTAAACACC 1563

Qy 661 AAG 663

Db 1564 AAG 1566

RESULT 10

ACD28901

ID ACD28901 standard; DNA; 1837 BP.

XX

AC ACD28901;

XX

DT 27-AUG-2003 (first entry)

XX

DE Streptococcus pyrogenic toxin a L42R mutant, DNA.

XX

KW SPEA; streptococcus pyrogenic enterotoxin a; gene; mutant; vaccine; ds;

KW superantigen toxin; MHC; superantigen-associated bacterial infection;

XX bacterial infection; antibacterial.

OS Streptococcus sp.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 814..1566

FT /tag= a

FT /product= "SPEA L42R"

FT sig_peptide 814..903

FT /tag= b

FT mat_peptide 904..1566

FT /tag= c

FT /label= Mature_SPEA_L42R

XX

PN US2003036544-A1.

XX

PD 20-FEB-2003.

XX

PF 26-NOV-2001; 2001US-00002784.

XX

PR 25-JUN-1997; 97US-00882431.

PR 01-SEP-1998; 98US-00144776.

XX

PA (ULRI/) ULRICH R G.

XX

PI Ulrich RG;

XX

DR WPI; 2003-492125/46

DR P-PSDB; ABU62331.

XX New superantigen toxin DNA fragment, useful for preparing a composition

PT for treating or preventing bacterial infection.

XX

PS Claim 4; Page 36-37; 68pp; English.

XX

CC The invention relates to an isolated and purified superantigen toxin DNA

CC fragment is altered so that binding of the encoded altered toxin to

CC either the MHC class II or T cell antigen receptor is altered. Also

CC included are a recombinant DNA construct (comprising a vector and an

CC isolated and purified altered superantigen toxin DNA fragment), a host

CC cell transformed with the recombinant DNA construct, producing altered

CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)

CC superantigen toxin peptide, diagnosing superantigen-associated bacterial

CC infection, a vaccine (comprising an altered superantigen toxin for

CC producing antigenic and immunogenic response resulting in the protection

CC of a mammal against superantigen-associated bacterial infection),

CC treating/ameliorating a superantigen-associated bacterial infection),

CC antiserum isolated from individuals immunised with one or more altered

CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-

CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,

CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and

CC SPEb).

XX

SQ Query Match 99.0%; Score 656.6; DB 8; Length 1837;

Best Local Similarity 99.4%; Pred. No. 1.8e-119;

Matches 659; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CACAAGACCCCGATCCAGCCAACTTACAGATCTAGTTAGTTAAACCTTCAAAAT 60

DB 904 CACAAGACCCCGATCCAGCCAACTTACAGATCTAGTTAGTTAAACCTTCAAAAT 963

QY 61 ATATATTTCTTTATGAGGTGACCTGTTACTACAGAGATGTGAATCTGTGTATCAA 120

DB 964 ATATATTTCTTTATGAGGTGACCTGTTACTACAGAGATGTGAATCTGTGTATCAA 1023

QY 121 CTTTATCTCACCATTAAATATATAATGTTTTCAGGGCCAAATATATGATAATTAATAA 180

DB 1024 CTTAGATCTCAGATTAAATATATAATGTTTTCAGGGCCAAATATATGATAATTAATAA 1083

QY 181 GAACCTTAAGAACCAAGAGATGGCACTTTATTTAAGGATATAAAGCTGTATTTATGGT 240

DB 1084 GAACCTTAAGAACCAAGAGATGGCACTTTATTTAAGGATATAAAGCTGTATTTATGGT 1143

QY 241 GTAGATATTTACCATCTCTGTTATTTATGTTGAAATGCAGAAAGGAGTGTATCTAC 300

DB 1144 GTAGATATTTACCATCTCTGTTATTTATGTTGAAATGCAGAAAGGAGTGTATCTAC 1203

QY 301 GGAGGGGTAAACAATCATAGGGAATCATTTAGAAATTCCTAAAGATAGTGTGTTAAA 360

DB 1204 GGAGGGGTAAACAATCATAGGGAATCATTTAGAAATTCCTAAAGATAGTGTGTTAAA 1263

QY 361 GTATCAATCATGATGATATCCAAAGCTATCATTTGATATTAAGAAATAAATAAATGGTA 420

DB 1264 GTATCAATCATGATGATATCCAAAGCTATCATTTGATATTAAGAAATAAATAAATGGTA 1323

QY 421 ACTGCTCAAGATTTAGACTATTAAGTTAGAAATATCTTACAGATATTAAGCAACTATAT 480

DB 1324 ACTGCTCAAGATTTAGACTATTAAGTTAGAAATATCTTACAGATATTAAGCAACTATAT 1383

QY 481 ACTAATGGACCTTCTAAATATGAAGTGGATATATAAAGTTTCATACCTAAGATAAGAA 540

DB 1384 ACTAATGGACCTTCTAAATATGAAGTGGATATATAAAGTTTCATACCTAAGATAAGAA 1443

QY 541 AGTTTGGTTGATTTTTTCCCTGAACCAAGATTTTACTCAATCAATAATCTTATGATA 600

DB 1444 AGTTTGGTTGATTTTTTCCCTGAACCAAGATTTTACTCAATCAATAATCTTATGATA 1503

QY 601 TATAAGATATTAAGACGCTTGACTCAAAACACAGCCAAATTTGAAGTCTTACCTAACCAACC 660

DB 1504 TATAAGATATTAAGACGCTTGACTCAAAACACAGCCAAATTTGAAGTCTTACCTAACCAACC 1563

QY 661 AAG 663

DB 1564 AAG 1566

RESULT 11

ACD28908

ID ACD28908 standard; DNA; 1419 BP.

XX ACD28908;

XX

DT 27-AUG-2003 (first entry)

XX

DE SPEa L42R/SPEb C47S mutant fusion protein, DNA.

XX

KW SPEa; streptococcus pyrogenic enterotoxin; gene; mutant; vaccine; ds;

KW superantigen toxin; MHC; superantigen-associated bacterial infection;

KW bacterial infection; antibacterial; SPEb.

XX

OS Streptococcus sp.

OS Synthetic.

XX

PH Key Location/Qualifiers

FT CDS 1. 1419

FT /tag= a

FT /product= "SPEa L42R/SPEb C47S"

FT /transl_except= (pos:298..306,aa:Ile-Gly)

FT /transl_except= (pos:634..642,aa:Thr-Gln)

FT /transl_except= (pos:1162..1170,aa:Ser-Gln)

FT /transl_except= (pos:1228..1236,aa:Gly-Gly)

XX

XX US2003036644-A1.

XX

PD 20-FEB-2003.

XX

PF 26-NOV-2001; 2001US-00002784.

XX

PA 25-JUN-1997; 97US-00882431.

PR 01-SEP-1998; 98US-00144776.

XX

XX (ULRI/) ULRICH R G.

XX

XX Ulrich RG;

DR WPI; 2003-492125/46.

DR P-PSDB; ABU62335.

XX

PT New superantigen toxin DNA fragment, useful for preparing a composition

PT for treating or preventing bacterial infection.

XX

XX Claim 6; Page 39-40; 68pp; English.

XX

CC The invention relates to an isolated and purified superantigen toxin DNA

CC fragment is altered so that binding of the encoded altered toxin to

CC either the MHC class II or T cell antigen receptor is altered. Also

CC included are a recombinant DNA construct (comprising a vector and an

CC isolated and purified altered superantigen toxin DNA fragment), a host

CC cell transformed with the recombinant DNA construct, producing altered

CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)

CC superantigen toxin peptide, diagnosing superantigen-associated bacterial

CC infection, a vaccine (comprising an altered superantigen toxin for

CC producing antigenic and immunogenic response resulting in the protection

CC of a mammal against superantigen-associated bacterial infection),

CC treating/ameliorating a superantigen-associated bacterial infection),

CC antiserum isolated from individuals immunised with one or more altered

CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-

CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,

CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and

CC SPB). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence encodes the SpeA L42R/SPB C47S mutant fusion protein
XX
SQ Sequence 1419 BP; 497 A; 266 C; 255 G; 401 T; 0 U; 0 Other;
Query Match 98.3%; Score 651.8; DB 8; Length 1419;
Best Local Similarity 98.9%; Pred. No. 1.6e-118;
Matches 656; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CAACAAGACCCCGATCCCAAGCCAACTTCACAGATCTAGTTTAAAGGATGCAAACTTCAAAAT 60
Db 4 CAACAAGACCCCGATCCCAAGCCAACTTCACAGATCTAGTTTAAAGGATGCAAACTTCAAAAT 63
QY 61 ATATATTTTCTTTATGAGGTTGACCTGTTACTACGAGATGCAAACTTCTGTTGATCAA 120
Db 64 ATATATTTTCTTTATGAGGTTGACCTGTTACTACGAGATGCAAACTTCTGTTGATCAA 123
QY 121 CTTTATCTCAACATTTAATATATATGTTTCAGGCGCAAACTTATGATAAATTTAAAAACT 180
Db 124 CTTGATCTCAGATTTAATATATATGTTTCAGGCGCAAACTTATGATAAATTTAAAAACT 183
QY 181 GAACCTTAAGAACCAAGAGATGCAAACTTTATTTAAGGATGCAAACTTCTGTTGATCAA 240
Db 184 GAACCTTAAGAACCAAGAGATGCAAACTTTATTTAAGGATGCAAACTTCTGTTGATCAA 243
QY 241 GTAGATATTTACCATCTCTGTTTATTTATGTAAGGATGCAAACTTCTGTTGATCAA 300
Db 244 GTAGATATTTACCATCTCTGTTTATTTATGTAAGGATGCAAACTTCTGTTGATCAA 303
QY 301 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTTAAAGATAGTCTGTTAAA 360
Db 304 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTTAAAGATAGTCTGTTAAA 363
QY 361 GTATCAATCGATGGTATCAAAAGCCTATCATTTGATATTTGAAACAAATTTAAAAATGGTA 420
Db 364 GTATCAATCGATGGTATCAAAAGCCTATCATTTGATATTTGAAACAAATTTAAAAATGGTA 423
QY 421 ACTGCTCAAGATTTAGACTATAAGTTAGAAATATCTTACAGATAATTAAGCACTATAT 480
Db 424 ACTGCTCAAGATTTAGACTATAAGTTAGAAATATCTTACAGATAATTAAGCACTATAT 483
QY 481 ACTAATGACCTTCTAAATATGAAATCGATATATAAGTTTCAATACCTAAGATTAAGAA 540
Db 484 ACTAATGACCTTCTAAATATGAAATCGATATATAAGTTTCAATACCTAAGATTAAGAA 543
QY 541 AGTTTGTGTTGATTTTTCCTGAAACAGAAATTTACTCAATCAAAATATCTTATGATA 600
Db 544 AGTTTGTGTTGATTTTTCCTGAAACAGAAATTTACTCAATCAAAATATCTTATGATA 603
QY 601 TATTAAGATTAAGAACTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCT 660
Db 604 TATTAAGATTAAGAACTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCT 663
QY 661 AAG 663
Db 664 AAG 666
RESULT 12
AAD56778
ID AAD56778 standard; DNA; 1419 BP.
XX
AC AAD56778;
XX
DT 06-OCT-2003 (first entry)
DE Streptococcus pyogenes SpeA-SpeB fusion DNA.
XX
KW Supranatigen toxin; vaccine; infection; pyrogenic exotoxin A; SpeA;
XX gene therapy; fusion protein; SpeB; gene; ds.
OS Streptococcus pyogenes.

XX Key Location/Qualifiers
FH CDS 1..1419
FT /*tag= a
FT /product= "S. pyogenes SpeA-SpeB fusion protein"
FT /transl_except= (pos:298..306, aa:Ile-Gly)
FT /transl_except= (pos:634..642, aa:Thr-Gln)
FT /transl_except= (pos:1162..1170, aa:Ser-Gln)
FT /transl_except= (pos:1228..1236, aa:Gly-Gly)
XX
PN WO2403056015-A1.
XX 10-JUL-2003.
XX 26-NOV-2001; 2001WO-US046540.
XX 26-NOV-2001; 2001US-00002784.
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX Ulrich RG;
XX WPI; 2003-492125/46.
XX P-PSDB; AAE37684.
XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX Claim 6; Page 132-133; 141pp; English.
XX The invention provides a superantigen toxin DNA fragment which has been
XX genetically altered such that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is disrupted or
XX altered. DNA fragments of the invention are useful in the production of
XX vaccines against bacterial superantigen toxin infections. They are also
XX useful in gene therapy. The present sequence is Streptococcus pyogenes
XX pyrogenic exotoxin A (SpeA)-SpeB fusion DNA. This sequence is used in the
XX invention
SQ Sequence 1419 BP; 497 A; 266 C; 255 G; 401 T; 0 U; 0 Other;
Query Match 98.3%; Score 651.8; DB 8; Length 1419;
Best Local Similarity 98.9%; Pred. No. 1.6e-118;
Matches 656; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CAACAAGACCCCGATCCCAAGCCAACTTCACAGATCTAGTTTAAAGGATGCAAACTTCAAAAT 60
Db 4 CAACAAGACCCCGATCCCAAGCCAACTTCACAGATCTAGTTTAAAGGATGCAAACTTCAAAAT 63
QY 61 ATATATTTTCTTTATGAGGTTGACCTGTTACTACGAGATGCAAACTTCTGTTGATCAA 120
Db 64 ATATATTTTCTTTATGAGGTTGACCTGTTACTACGAGATGCAAACTTCTGTTGATCAA 123
QY 121 CTTTATCTCAACATTTAATATATATGTTTCAGGCGCAAACTTATGATAAATTTAAAAACT 180
Db 124 CTTGATCTCAGATTTAATATATATGTTTCAGGCGCAAACTTATGATAAATTTAAAAACT 183
QY 181 GAACCTTAAGAACCAAGAGATGCAAACTTTATTTAAGGATGCAAACTTCTGTTGATCAA 240
Db 184 GAACCTTAAGAACCAAGAGATGCAAACTTTATTTAAGGATGCAAACTTCTGTTGATCAA 243
QY 241 GTAGATATTTACCATCTCTGTTTATTTATGTAAGGATGCAAACTTCTGTTGATCAA 300
Db 244 GTAGATATTTACCATCTCTGTTTATTTATGTAAGGATGCAAACTTCTGTTGATCAA 303
QY 301 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTTAAAGATAGTCTGTTAAA 360
Db 304 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTTAAAGATAGTCTGTTAAA 363
QY 361 GTATCAATCGATGGTATCAAAAGCCTATCATTTGATATTTGAAACAAATTTAAAAATGGTA 420
Db 364 GTATCAATCGATGGTATCAAAAGCCTATCATTTGATATTTGAAACAAATTTAAAAATGGTA 423

QY 421 ACTGCTCAAGATTAGACTATTAAGTTAGAAATATCTTACAGATAAAGCAACTATAT 480
 Db |||||
 QY 424 ACTGCTCAAGATTAGACTATTAAGTTAGAAATATCTTACAGATAAAGCAACTATAT 483
 Db |||||
 QY 481 ACTATGACCTTCTAATATGAATCTGAATATAAAGTTCTATACCTAAGATAAGAA 540
 Db |||||
 QY 484 ACTAATGACCTTCTAATATGAATCTGAATATAAAGTTCTATACCTAAGATAAGAA 543
 Db |||||
 QY 541 AGTTTTCGTTGATTTTTCCTCGAACCCAGAAATTTACTCAATCTAATATCTTATGATA 600
 Db |||||
 QY 544 AGTTTTCGTTGATTTTTCCTCGAACCCAGAAATTTACTCAATCTAATATCTTATGATA 603
 Db |||||
 QY 601 TATAAGATAAATGAACCGTTGACTCAACACAGCCAAATGGAAGTCTACCTAACACC 660
 Db |||||
 QY 604 TATAAGATAAATGAACCGTTGACTCAACACAGCCAAATGGAAGTCTACCTAACACC 663
 Db |||||
 QY 661 AAG 663
 Db |||||
 QY 664 AAG 666

RESULT 13

ACA64700
 ID ACA64700 standard; DNA; 1031 BP.

XX ACA64700;

DT 18-JUN-2003 (first entry)

DE S. Pyogenes exotoxin (SPEA) gene.

XX Superantigen; ds; gene; SAG; staphylococcal enterotoxin; tumour; cancer;
 KW apoptosis; gene therapy; mammalian cell receptor; cytostatic;
 KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
 KW tumouricidal immunocyte; anti-tumour.

XX Streptococcus pyogenes.

XX US2002177551-A1.

XX 28-NOV-2002.

XX 30-MAY-2001; 2001US-00870759.

XX 31-MAY-2000; 2000US-0208128P.

XX (TERM/) TERMAN D S.

XX Terman DS;

XX WPI; 2003-361759/34.

XX P-PSDB; ABU79074.

XX A mammalian cell receptor, useful in the treatment of cancer by binding
 to tumor associated lipids where the binding induces anergy or apoptosis
 in T cells and antigen presenting cells.

XX Disclosure; Page: 167pp; English.

XX The invention relates to a mammalian cell receptor, useful in the
 treatment of cancer, which binds to tumour associated lipids and induces
 anergy or apoptosis in the T cells and antigen presenting cells (APCs).
 XX Also included are a mammalian cell useful in the treatment of cancer
 where the receptor which binds tumour associated lipids and induces
 cellular inactivation or death is deleted or functionally deactivated,
 producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 (by allowing tumour associated lipids to contact immunocytes in which
 receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
 sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 deleted), a construct useful in the treatment of cancer comprising a
 superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 useful in the treatment of cancer (where an adaptor protein which

CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidally
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to
 CC contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidally activated population,
 CC and administering APCs to the host), producing a tumouricidal T cell
 CC population ex vivo in a mammal (by allowing a tumour associated lipids to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC administering the tumouricidally activated T cells to the host, or
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidally activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC receptors, methods and compositions are useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence encodes a bacterial superantigen protein (e.g. a staphylococcal
 CC enterotoxin). Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format from
 CC the US patent office website at
 CC "seqdata.uspto.gov/sequence.html?DocID=20020177551"

XX SQ Sequence 1031 BP; 381 A; 146 C; 162 G; 342 T; 0 U; 0 Other;

Query Match 87.9%; Score 582.6; DB 7; Length 1031;

Best Local Similarity 97.1%; Pred. No. 5.3e-105;

Matches 636; Conservative 0; Mismatches 14; Indels 5; Gaps 4;

QY 10 CCGGATCCAGCCCAACTTCCAGATCTAGTTAGTTAAACCTTCAAAATATATATTTT 69

Db ||||| 178 CCCAAGCCCGCCCAATACAAAGATCTAATTTAGTT-AAAACCTTCAAAATATATATTTT 236

QY 70 CTTTATGAGGGTGACCCCT-GTTACTCACGAGATGTGAAATCTCTGATCAACTTTTATC 128

Db ||||| 237 CTTTATGAGGGTGACCCCTGTTACTCACGAGATGTGAAATCTCTGATCAACTTTTATC 296

QY 129 TCACCATTTAATATAATGTTTCAGGGCCAAATTTATGATAAAATATAAACTGAACCTAA 188

Db ||||| 297 ACACGATTTAATATAATGTTTCAGGGCCAAATTTATGATAAAATATAAACTGAACCTAA 356

QY 189 GAACCAAGAGATGCGCACTTTATTAGGATAAAACGTTGATATTTTATGTTAGATA 248

Db ||||| 357 GAACCAAGAGATGCGCACTTTATTAGGATAAAACGTTGATATTTTATGTTAGATA 416

QY 249 TTACCATCTCTGTTATTATTATGTGAAATGAGAGGATGTCATCTACCGAGGGGT 308

Db ||||| 417 TTACCATCTCTGTTATTATTATGTGAAATGAGAGGATGTCATCTACCGAGGGGT 476

QY 309 AACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAAGTATCAAT 368

Db ||||| 477 AACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAAGTATCAAT 536

QY 369 CGATGGTATCCAAAGCCTATCTTTCATTTGAAACAAATATAAAATATGTAATCTGCTCA 428

Db ||||| 537 CGATGGTATCCAAAGCCTATCTTTCATTTGAAATATAAAATATGTAATCTGCTCA 594

QY 429 AGAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATAACCACTATATATACTATGG 488

Db ||||| 595 AGAATTAG-CTATACAGTTAGAAAATATCTTACAGATAATAACCACTATATATACTATGG 653

QY 489 ACCTTCTAAATATGAACTGGATATATATAAGTTCTACCTAAGATAAAGAAAGTTTGTG 548
 Db 654 ACCTTCTAAATATGAACTGGATATATATAAGTTCTACCTAAGATAAAGAAAGTTTGTG 713
 QY 549 GTTTCATTTTCCCTGACCAAGAAATTTACTCAATCTAAATATCTTATGATATATAAGA 608
 Db 714 GTTTCATTTTCCCTGACCAAGAAATTTACTCAATCTAAATATCTTATGATATATAAGA 773
 QY 609 TAATGAAACGGTTGACTCAACACCAAGCCAAATTTGAAGTCTACCTAACCAACCAAG 663
 Db 774 TAATGAAACGGTTGACTCAACACCAAGCCAAATTTGAAGTCTACCTAACCAACCAAG 828
 RESULT 14
 ACA64696
 ID ACA64696 standard; DNA; 1095 BP.
 XX
 AC ACA64696;
 XX
 DT 18-JUN-2003 (first entry)
 XX
 DE S. aureus SEC (staphylococcus enterotoxin C) gene.
 XX
 KW Superantigen; ds; gene; SAG; staphylococcal enterotoxin; tumour; cancer;
 KW apoptosis; gene therapy; mammalian cell receptor; cytostatic;
 KW tumour associated lipid; energy; T cell; antigen presenting cell; APC;
 KW tumouricidal immunocyte; antitumour.
 XX
 OS Staphylococcus aureus.
 XX
 PN US2002177551-A1.
 XX
 PD 28-NOV-2002.
 XX
 XX 30-MAY-2001; 2001US-00870759.
 PF
 XX 31-MAY-2000; 2000US-0208128P.
 PR
 XX (TERM/) Terman D S.
 PA
 XX Terman DS;
 PI
 XX WPI; 2003-361759/34.
 DR P-PSDB; ABU79070.
 XX
 PT A mammalian cell receptor, useful in the treatment of cancer by binding
 PT to tumor associated lipids where the binding induces energy or apoptosis
 PT in T cells and antigen presenting cells.
 PT
 XX Disclosure; Page; 167pp; English.
 XX
 CC The invention relates to a mammalian cell receptor, useful in the
 CC treatment of cancer, which binds to tumour associated lipids and induces
 CC energy or apoptosis in the T cells and antigen presenting cells (APCs).
 CC Also included are a mammalian cell useful in the treatment of cancer
 CC where the receptor which binds tumour associated lipids and induces
 CC cellular inactivation or death is deleted or functionally deactivated,
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 CC (by allowing tumour associated lipids to contact immunocytes in which
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 CC sphingolipids, glycosphingolipids, phosphoglycolipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 CC deleted), a construct useful in the treatment of cancer comprising a
 CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 CC useful in the treatment of cancer (where an adaptor protein which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidal

activated immunocytes to the host), producing (M3) a tumouricidal APC
 population ex vivo in a mammal (by allowing a tumour associated lipid to
 contact APCs, in which receptors for the tumour associated lipids are
 inactivated or deleted to produce a tumouricidally activated population,
 and administering APCs to the host), producing a tumouricidal T cell
 population ex vivo in a mammal) by allowing a tumour associated lipids to
 contact T cells, in which adaptor proteins, which inhibit T cell
 activation by tumour associated antigens, are deleted or functionally
 deactivated to produce a tumouricidal population of T cells, and
 administering the tumouricidally activated T cells to the host, or
 allowing a superantigen-lipid raft to contact T cells ex vivo, and
 administering the tumouricidally activated T cells to the host), treating
 (M5) cancer in a mammal (by administering a lipid binding molecule which
 binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 a tumouricidal T cell population in vivo in a mammal (by allowing a
 tumour associated antigen to contact immunocytes in which adaptor
 proteins which inhibit T cell activation by tumour associated antigens
 are deleted or functionally deactivated) and producing (M7) a
 tumouricidal T cell population ex vivo in a mammal comprising allowing a
 superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 receptors methods and compositions are co-administered or administered as
 tumours. Bacterial superantigens are co-administered or administered as
 fusion constructs with anti-tumour proteins or motifs. The present
 sequence encodes a bacterial superantigen protein (e.g. a staphylococcal
 enterotoxin). Note: The sequence data for this patent did not form part
 of the printed specification, but was obtained in electronic format from
 the US patent office website at
 "seqdata.uspto.gov/sequence.html?DocID=20020177551"
 XX
 SQ Sequence 1095 BP; 433 A; 125 C; 185 G; 352 T; 0 U; 0 Other;
 Query Match 25.2%; Score 167.4; DB 7; Length 1095;
 Best Local Similarity 59.0%; Pred. No. 1e-23;
 Matches 382; Conservative 0; Mismatches 226; Indels 39; Gaps 4;
 QY 56 AAAATATATATTTCTTTATGAGGGTGACCCCTGTACTCAGAGATGTGAATCTGTG 115
 Db 263 AAAATATGAAAGTTTATATGATGATCATTTATGATATCAGCAACTAAGTTAAGTCTGTAG 322
 QY 116 ATCAACTTTTATCTCACCATTAAATATATAATGTTTTCAGG-----GCCAAATATAG 166
 Db 323 ATAAATTTTGGCACATGATTTTAAATTTTAACTAGTATGATAAACAATGAAATATAG 382
 QY 167 ATAAATTTAAACTGAACTTAAGAACCAAGAGATGCAACTTTTATTTAAGGATAAACAAG 226
 Db 383 ACRAAGTGAACACAGAGTTTATTAAATGAAGTTTAGCAAGAGTACAAAGATGAAGTAG 442
 QY 227 TTGATATTTATGTTGATGAGATATTTACCATCTCTGTTATTTAT----- 268
 Db 443 TTGATGTGTATGATCAAAATTTACTATGTAACCTGCTATTTTTCATCCAAGATAATGTAG 502
 QY 269 GTGAAATCGAAGAGAGTGCATGTATCTACGAGGGGTAAACAAATCATGAAGGAATC 328
 Db 503 GTAAAGTTACAGGTGCAAAACTTGTATGTATGGAGGAATACAAACAATGAAGGAACC 562
 QY 329 ATTAGAAATTCCTA-----AAAAGATAGTCGTTTAAGATGATCAATCGATGGTATCCAAA 382
 Db 563 ACTTTGATATGGAAGTTTACAAATGTACTTATAAGAGTTTATGAAATATAAAGAAACA 622
 QY 383 GCCTATCTTTGATATGAAACAAATAAANAATGTTAACTGCTCAAGATTAAGACTATA 442
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 QY 443 AAGTTAGAAATATCTTACAGATAATAAGCAACTATATATAATGGAACCTCTTAATATG 502
 Db 683 AAGCTAGGAATTTTAAATTAATAAANAATTTGTATGAGTTTAAACAGTTCCACCATATG 742
 QY 503 AAACCTGGATATATAAAGTTTCATACCTAAGATAAAGAAAGTTTTCGTTGATTTTTC 562
 Db 743 AAACAGGATATATAAATTTTATTTGAAATAAACCGCAATACTTTTTCGTATGATATGATGC 802
 QY 563 CTGAACGAG-----AATTTACTCAATCTAAATATCTTATGATATATAAAGATAATGAAA 616

Db 803 CTGACAGGCGATAAGTTTGACCAATCTAAATATTTAATGATGTACAAACGACATATAAA 862
 QY 617 GCCTTGACTCAACACACAGCCAAATTTGAAGTCTACTACCTAACACCAAG 663
 Db 863 CGGTGTGATCTAAAGTGTGAAGATAGAGATCCACCTTACACCAAG 909
 RESULT 15
 AAT45698
 ID AAT45698 standard; cDNA; 773 BP.
 XX
 AC AAT45698;
 XX
 DT 08-MAR-1997 (first entry)
 XX
 DE Staphylococcus enterotoxin B cDNA.
 XX
 KW Enterotoxin B; SEB; superantigen; antigen; cytokine; chemokine; T cell;
 KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;
 KW adjuvant; ss.
 XX
 OS Staphylococcus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..768
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 FT /note= "the full-length coding sequence can be used in
 FT nucleic acid-based therapeutic compsns. of the invention"
 FT 1..45
 FT sig_peptide
 FT /*tag= b
 FT complement (37..61)
 FT /*tag= d
 FT /note= "SEB.S amplification primer binding site"
 FT 46..765
 FT mat_peptide
 FT /*tag= c
 FT /note= "the coding sequence for the mature protein can be
 FT used in nucleic acid-based therapeutic compsns. of the
 FT invention"
 FT 754..768
 FT primer_bind
 FT /*tag= e
 FT /note= "SEB.S amplification primer binding site"
 FT
 XX WO9636366-A1.
 XX
 XX 21-NOV-1996.
 XX
 XX 20-MAY-1996; 96WO-US007432.
 XX
 XX 18-MAY-1995; 95US-00446918.
 XX 29-DEC-1995; 95US-00580806.
 XX
 XX (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
 XX
 XX Dow SW, Elmslie RE, Potter TA;
 XX WPI; 1997-011857/01.
 XX P-PSDB; AAW06737.
 XX
 XX Recombinant molecule encoding super:antigen and opt. cytokine or
 XX chemokine - controls activity of effector cells (T cells, monocytes,
 XX natural killer cells), used for gene therapy of cancer.
 XX
 XX Example 1; Page 95-96; 131pp; English.
 XX
 CC A cDNA clone (AAT45698) codes for staphylococcal enterotoxin B (AAW06737)
 CC superantigen. Nucleic acids encoding superantigens (see also AAT45699 and
 CC AAT45706) can be utilised in the gene therapy of cancer, infectious
 CC diseases and immunological disorders. The nucleic acid, optionally in
 CC combination with cytokine or chemokine nucleic acids, is delivered to an
 CC animal using e.g. liposomes. It acts by controlling the activity of
 CC effector cells, such as T-cells, macrophages, monocytes and/or natural
 CC killer cells. Localised prodn. of an effective but non-toxic amount of
 CC encoded proteins allows safe treatment of the animal. Adjuvants

CC comprising an immunogen and a superantigen nucleic acid can be used with
 CC DNA- based vaccines
 XX
 SQ Sequence 773 BP; 305 A; 94 C; 133 G; 241 T; 0 U; 0 Other;
 Query Match 25.2%; Score 166.8; DB 2; Length 773;
 Best Local Similarity 59.1%; Pred. No. 1.3e-23;
 Matches 384; Conservative 0; Mismatches 221; Indels 45; Gaps 4;
 QY 56 AAAATATATATTTCTTTTATGAGGTCACCCCTGTTACTCAGAGAATGTGAAATCTGTTG 115
 Db 113 AAAATATGAAAGTTTGTGATGATGATATCATGTCATGATCAGCAATAAACCTTAAATCTATAG 172
 QY 116 ATCAACTTTTATCTCACCAATTTAATATATAATGTTTCAGGGCCA-----AATTATG 166
 Db 173 ATCAATTTCTATCTTTGACTTAAATATCTTATTAAGGACACTAAGTTAGGGAATATG 232
 QY 167 ATAAATTAATAAAGTAAAGTAAAGCAAGAGATGGCAACTTTTATTTAAGGATAAACG 226
 Db 233 ATAATGTTTCGAGTCGAATTTAAACCAAGAAATTTAGCTGATATAATACAAAGATAAATACG 292
 QY 227 TTGATATTTATGTTGTAGAAATATTACCATCTCTCTGTTATTTATGTGAAAA----- 275
 Db 293 TAGATGTTTGGAGCTAATTTATTTATCAATGTTATTTTCTTAAAAAACGATGATA 352
 QY 276 -----TGCAGAAAGGAGTGTCATCTCTACGAGGGGTATCAACAAATTAGACT 439
 Db 353 TTAATTCGCATCAAACTGACAAACGAAAACTTGTATGTTATGTTGTTAACTGAGCATA 412
 QY 320 AAGGGAATCATTTAGAAATTCCTAAAAGATAGTCGTTAAAGTATCAATCGATGTTATCC 379
 Db 413 ATGGAACCAATTTAGATAAATAATAGAAATTTACTGTTCCGGTATTTGAAGATGGTAAAA 472
 QY 380 AAAGCCTTATCATTTTGATATTGAAACAAATAAAAAATGGTAACTGCTCAAGAAATTAGACT 439
 Db 473 ATTTATTTATCTTTTGACGTACAACTAATAAGAAAAAGGTGACTGCTCAAGAAATTAGATT 532
 QY 440 ATAAAGTTAGAAATATCTTTACAGATAATAAGCAACTATATATACTAAATGGACCTTTCTAAAT 499
 Db 533 ACCTAACTCGTCATTTTGGTGAATAAATAAACTCTATGAATTTTAAACAACTCGCCTT 592
 QY 500 ATGAACTGGATATATAAAGTTCTATACCTAAGATAAAGAAAGTTTGGTTGATGATTTT 559
 Db 593 ATGAAACGGATATATTAAATTTTAATA-----GAAATGAGATAGCTTTTGGTATGACATGA 649
 QY 560 TCCTGAACCAAG-----AAATTTACTCAATCTAAATCTTTATGATATATAAAGATATG 613
 Db 650 TGCTGCACCAAGGAGATAAATTTGACCAATCTAAATTTAAATGATGTACATGACATATA 709
 QY 614 AAACGCTTGACTCAACACAAAGCCAAATTTGAAGTCTACCTTAAACCAAG 663
 Db 710 AAATGGTTGATTTCTAAAGATGTGAAGATTGAAGTTTATCTTACGACAAAG 759

Search completed: September 3, 2004, 17:26:20
 Job time : 377 secs

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OM nucleic - nucleic search, using sw model

Run on: September 3, 2004, 18:16:37 : Search time 422 Seconds
(without alignments)
7809.322 Million cell updates/sec

Title: US-10-625-221-12_COPY_918_1580

Perfect score: 663

Sequence: 1 caacaagaccccgatcaag.....aagttacttaacaacccaag 663

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Gapop 10.0 , Gapext 1.0

Searched: 3267054 seqs, 2485319735 residues

Total number of hits satisfying chosen parameters: 6534108

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
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5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	663	100.0	1851	8	US-08-973-391A-12
2	663	100.0	1851	13	US-09-308-830-12
3	661.4	99.8	1837	9	US-09-452-599-33
4	661.4	99.8	1837	15	US-10-121-120-33
5	658.2	99.3	1837	8	US-08-882-431-15
6	656.6	99.0	1837	15	US-10-002-784A-15
7	651.8	98.3	1419	15	US-10-002-784A-23
8	582.6	87.9	1031	9	US-09-870-759-19
9	582.6	87.9	1031	10	US-09-751-708A-19
10	167.4	25.2	1095	9	US-09-870-759-11
11	167.4	25.2	1095	10	US-09-751-708A-11
12	166.8	25.2	773	13	US-10-354-948-1
13	166.8	25.2	801	9	US-09-870-759-1
14	166.8	25.2	801	10	US-09-751-708A-1

Sequence 2, Appli
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Sequence 5, Appli
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Sequence 1, Appli
Sequence 887, App
Sequence 116, App
Sequence 986, App
Sequence 1, Appli

15 166.8 25.2 886 9 US-09-870-759-2
16 166.8 25.2 886 10 US-09-751-708A-2
17 166.8 25.2 1712 8 US-08-882-431-5
18 166.8 25.2 1712 9 US-09-870-759-9
19 166.8 25.2 1712 10 US-09-751-708A-9
20 166.8 25.2 1712 15 US-10-002-784A-5
21 164.2 24.8 1095 8 US-08-882-431-13
22 164.2 24.8 1095 15 US-10-002-784A-13
23 158.8 24.0 723 16 US-10-405-871-3
24 158.8 24.0 801 16 US-10-405-871-2
25 158.8 24.0 1388 8 US-08-882-431-9
26 158.8 24.0 1388 15 US-10-002-784A-9
27 158.8 24.0 1712 8 US-08-882-431-7
28 158.8 24.0 1712 15 US-10-002-784A-7
29 112 16.9 815 15 US-10-151-336-7
30 96.6 14.6 1136 9 US-09-870-759-13
31 96.6 14.6 1136 10 US-09-751-708A-13
32 79 11.9 1443 9 US-09-870-759-7
33 79 11.9 1443 10 US-09-751-708A-7
34 71 10.7 757 8 US-08-882-431-3
35 71 10.7 757 15 US-10-002-784A-3
36 71 10.7 757 16 US-10-405-871-1
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39 71 10.7 830 8 US-08-882-431-1
40 71 10.7 830 15 US-10-002-784A-1
41 66.2 10.0 675 8 US-08-781-986A-887
42 66.2 10.0 675 13 US-10-329-624-887
43 62.2 9.4 1789 9 US-09-939-980-116
44 60.8 9.2 7597 15 US-10-311-455-986
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c 45 9.1 3673778 15 US-10-312-841-1

ALIGNMENTS

RESULT 1

US-08-973-391A-12
; Sequence 12, Application US/08973391A
; Publication No. US20020054887A1
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Maruella
; APPLICANT: Stoehrt, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391A
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (828)..(1583)
; OTHER INFORMATION:
US-08-973-391A-12

Query Match 100.0%; Score 663; DB 8; Length 1851;

Best Local Similarity 100.0%; Pred. No. 2.4e-117; Indels 0; Gaps 0;
Matches 663; Conservative 0; Mismatches 0;

Qy 1 CAACAAGACCCCGATCAAGCCAACTTACAGATCTAGTTAGTTAAACCTTCAAAAT 60

Db 918 CAACAAGACCCCGATCAAGCCAACTTACAGATCTAGTTAGTTAAACCTTCAAAAT 977

QY 61 ATATATTTCTTTATGAGGGTGACCTGTTACTACGAGAAATGTGAATCTCTGTATCAA 120
DB |||||||
QY 978 ATATATTTCTTTATGAGGGTGACCTGTTACTACGAGAAATGTGAATCTCTGTATCAA 1037
DB |||||||
QY 121 CTTTATCTCACCATTATATATATATATGTTTTCAGGGCCAAATATGATAAAATAAAACT 180
DB |||||||
QY 1038 CTTTATCTCACCATTATATATATATGTTTTCAGGGCCAAATATGATAAAATAAAACT 1097
DB |||||||
QY 161 GAACCTTAAGAACCAAGAGATGCAACTTTATTTAAGGATAAAAAAGTTGATATTTATGGT 240
DB |||||||
QY 1098 GAACCTTAAGAACCAAGAGATGCAACTTTATTTAAGGATAAAAAAGTTGATATTTATGGT 1157
DB |||||||
QY 241 GTAGATATTTACCATCTCTGTTATTTATGTTGAATGCAAGAGAGTGCATGTTATCTAC 300
DB |||||||
QY 1158 GTAGATATTTACCATCTCTGTTATTTATGTTGAATGCAAGAGAGTGCATGTTATCTAC 1217
DB |||||||
QY 301 GGAGGGGTAAACAAATCATGAAGGGAATCAATTTAGAAATTCCTTAAAAAGATAGTCGTTAAA 360
DB |||||||
QY 1218 GGAGGGGTAAACAAATCATGAAGGGAATCAATTTAGAAATTCCTTAAAAAGATAGTCGTTAAA 1277
DB |||||||
QY 361 GTATCAATCGATGGTATCCAAAGCCATCAATTTGATATGAAACAAATAAAAATGGTA 420
DB |||||||
QY 1278 GTATCAATCGATGGTATCCAAAGCCATCAATTTGATATGAAACAAATAAAAATGGTA 1337
DB |||||||
QY 421 ACTGCTCAAGATTAAGACTTAAAGTTAGAAATATATTTAGAAATTCCTTAAAAAGATAGTCGTTAAA 480
DB |||||||
QY 1338 ACTGCTCAAGATTAAGACTTAAAGTTAGAAATATATTTAGAAATTCCTTAAAAAGATAGTCGTTAAA 1397
DB |||||||
QY 481 ACTAATGGAACCTTCTAAATATGAAACTGGATATATAAGTTTCATACCTTAAGAAATAAGAA 540
DB |||||||
QY 1398 ACTAATGGAACCTTCTAAATATGAAACTGGATATATAAGTTTCATACCTTAAGAAATAAGAA 1457
DB |||||||
QY 541 AGTTTGTGTTTCAATTTTTCCTGTAACAGAAATTTACTCAATCTAAATATCTTATGATA 600
DB |||||||
QY 1458 AGTTTGTGTTTCAATTTTTCCTGTAACAGAAATTTACTCAATCTAAATATCTTATGATA 1517
DB |||||||
QY 601 TATAAGATATGAAGCGTTGACTCAACACAGCCAAATGAAAGTCTACCTAACACACC 660
DB |||||||
QY 1518 TATAAGATATGAAGCGTTGACTCAACACAGCCAAATGAAAGTCTACCTAACACACC 1577
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QY 661 AAG 663
DB 1578 AAG 1580

RESULT 2

US-09-308-830-12
; Sequence 12, Application US/09308830
; Publication No. US20020086813A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould P.C.
; STREET: P.O. Box 2503
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402-0903
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/308,830
; FILING DATE: 04-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/22228
; FILING DATE: 05-DEC-1997

APPLICATION NUMBER: 60/032,930
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Skoog, Mark T
REGISTRATION NUMBER: 40,178
REFERENCE/DOCKET NUMBER: 600,346USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 828..1580
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-308-830-12

Query Match 100.0%; Score 663; DB 13; Length 1851;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAACAAGACCCGATCCAAAGCCAACTTCAAGATCTAGTTTAGTTTAAACCTTCAAAT 60
DB |||||||
QY 918 CAACAAGACCCGATCCAAAGCCAACTTCAAGATCTAGTTTAGTTTAAACCTTCAAAT 977
DB |||||||
QY 61 ATATATTTCTTTATGAGGGTGACCTGTTACTACGAGAAATGTGAATCTCTGTATCAA 120
DB |||||||
QY 978 ATATATTTCTTTATGAGGGTGACCTGTTACTACGAGAAATGTGAATCTCTGTATCAA 1037
DB |||||||
QY 121 CTTTATCTCACCATTATATATATATGTTTTCAGGGCCAAATATGATAAAATAAAACT 180
DB |||||||
QY 1038 CTTTATCTCACCATTATATATATGTTTTCAGGGCCAAATATGATAAAATAAAACT 1097
DB |||||||
QY 181 GAACCTTAAGAACCAAGAGATGCAACTTTATTTAAGGATAAAAAAGTTGATATTTATGGT 240
DB |||||||
QY 1098 GAACCTTAAGAACCAAGAGATGCAACTTTATTTAAGGATAAAAAAGTTGATATTTATGGT 1157
DB |||||||
QY 241 GTAGATATTTACCATCTCTGTTATTTATGTTGAATGCAAGAGAGTGCATGTTATCTAC 300
DB |||||||
QY 1158 GTAGATATTTACCATCTCTGTTATTTATGTTGAATGCAAGAGAGTGCATGTTATCTAC 1217
DB |||||||
QY 301 GGAGGGGTAAACAAATCATGAAGGGAATCAATTTAGAAATTCCTTAAAAAGATAGTCGTTAAA 360
DB |||||||
QY 1218 GGAGGGGTAAACAAATCATGAAGGGAATCAATTTAGAAATTCCTTAAAAAGATAGTCGTTAAA 1277
DB |||||||
QY 361 GTATCAATCGATGGTATCCAAAGCCATCAATTTGATATGAAACAAATAAAAATGGTA 420
DB |||||||
QY 1278 GTATCAATCGATGGTATCCAAAGCCATCAATTTGATATGAAACAAATAAAAATGGTA 1337
DB |||||||
QY 421 ACTGCTCAAGATTAAGACTTAAAGTTAGAAATATCTTACAGATAAATGAAGCAACTATAT 480
DB |||||||
QY 1338 ACTGCTCAAGATTAAGACTTAAAGTTAGAAATATCTTACAGATAAATGAAGCAACTATAT 1397
DB |||||||
QY 481 ACTAATGGAACCTTCTAAATATGAAACTGGATATATAAGTTTCATACCTTAAGAAATAAGAA 540
DB |||||||
QY 1398 ACTAATGGAACCTTCTAAATATGAAACTGGATATATAAGTTTCATACCTTAAGAAATAAGAA 1457
DB |||||||
QY 541 AGTTTGTGTTTCAATTTTTCCTGTAACAGAAATTTACTCAATCTAAATATCTTATGATA 600
DB |||||||
QY 1458 AGTTTGTGTTTCAATTTTTCCTGTAACAGAAATTTACTCAATCTAAATATCTTATGATA 1517
DB |||||||
QY 601 TATAAGATATGAAGCGTTGACTCAACACAGCCAAATGAAAGTCTACCTAACACACC 660
DB |||||||
QY 1518 TATAAGATATGAAGCGTTGACTCAACACAGCCAAATGAAAGTCTACCTAACACACC 1577
DB |||||||
QY 661 AAG 663

Db 1578 AAG 1580
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1444 AGTTTGGTTGATTTTCCCTGAACCAAGATTCTCAATCTAAATATCTTATGATA 1503
Qy 601 TATAAGATAATGAAAGCGTTGACTCAAAACACAGCAAAATGAGTCTACTTACCAACC 660
1504 TATAAGATAATGAAAGCGTTGACTCAAAACACAGCAAAATGAGTCTACTTACCAACC 1563
Qy 661 AAG 663
1564 AAG 1566
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RESULT 4
US-10-121-120-33
; Sequence 33, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 08/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-10-121-120-33

Query Match 99.8%; Score 661.4; DB 15; Length 1837;
Best Local Similarity 99.8%; Pred. No. 4.9e-117;
Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAACAAGACCCCGATCCAGCCAACTTCAAGATCTAGTTAGTTAAACCTTCAAAAT 60
Db 904 CAACAAGACCCCGATCCAGCCAACTTCAAGATCTAGTTAGTTAAACCTTCAAAAT 963
Qy 61 ATATATTTCTTTATGAGGTGACCTGTTACTCAGAGATGTGAATCTGTTGATCAA 120
Db 964 ATATATTTCTTTATGAGGTGACCTGTTACTCAGAGATGTGAATCTGTTGATCAA 1023
Qy 121 CTTTATCTCACCATTAAATATAATAATGTTTCAGGGCCAAATTTATGATAATTAATAACT 180
Db 1024 CTTTATCTCAGGATTTAATAATAATGTTTCAGGGCCAAATTTATGATAATTAATAACT 1083
Qy 181 GAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATATAAAACGTTGATTTGGT 240
Db 1084 GAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATATAAAACGTTGATTTGGT 1143
Qy 241 GTAGAAATTTACCAATCTCTGTTATTTATGTAAGATGCAAAAGAGTGTGATCTAC 300
Db 1144 GTAGAAATTTACCAATCTCTGTTATTTATGTAAGATGCAAAAGAGTGTGATCTAC 1203
Qy 301 GGAGGGGTAAACAATCATGAGGGAATCAATTTAGAAATTTCTTAAAGATAGTCTGTTAA 360
Db 1204 GGAGGGGTAAACAATCATGAGGGAATCAATTTAGAAATTTCTTAAAGATAGTCTGTTAA 1263
Qy 361 GTATCAATTCGATGGTATCCAAAGCCTATCTTTGATATTGAAAACAAATATAAAATGGTA 420
Db 1264 GTATCAATTCGATGGTATCCAAAGCCTATCTTTGATATTGAAAACAAATATAAAATGGTA 1323
Qy 421 ACTGCTCAAGAAATAGACTATAAAGTTAGAAAAATCTTTAAGATTAAGCAACTATAT 480
Db 1324 ACTGCTCAAGAAATAGACTATAAAGTTAGAAAAATCTTTAAGATTAAGCAACTATAT 1383
Qy 481 ACTAATGACCTCTTAATATCAACTGGATATATTAAGTTTCACTACCTAAGAAATAAGAA 540
Db 1384 ACTAATGACCTCTTAATATCAACTGGATATATTAAGTTTCACTACCTAAGAAATAAGAA 1443
Qy 541 AGTTTGGTTGATTTTCCCTGAACCAAGATTTTACTCAATCTTAAATATCTTATGATA 600
|||

Db 1578 AAG 1580
|||
1444 AGTTTGGTTGATTTTCCCTGAACCAAGATTCTCAATCTAAATATCTTATGATA 1503
Qy 601 TATAAGATAATGAAAGCGTTGACTCAAAACACAGCAAAATGAGTCTACTTACCAACC 660
1504 TATAAGATAATGAAAGCGTTGACTCAAAACACAGCAAAATGAGTCTACTTACCAACC 1563
Qy 661 AAG 663
1564 AAG 1566
|||

RESULT 3
US-09-452-599-33
; Sequence 33, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-09-452-599-33

Query Match 99.8%; Score 661.4; DB 9; Length 1837;
Best Local Similarity 99.8%; Pred. No. 4.9e-117;
Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAACAAGACCCCGATCCAGCCAACTTCAAGATCTAGTTAGTTAAACCTTCAAAAT 60
Db 904 CAACAAGACCCCGATCCAGCCAACTTCAAGATCTAGTTAGTTAAACCTTCAAAAT 963
Qy 61 ATATATTTCTTTATGAGGTGACCTGTTACTCAGAGATGTGAATCTGTTGATCAA 120
Db 964 ATATATTTCTTTATGAGGTGACCTGTTACTCAGAGATGTGAATCTGTTGATCAA 1023
Qy 121 CTTTATCTCACCATTAAATATAATAATGTTTCAGGGCCAAATTTATGATAATTAATAACT 180
Db 1024 CTTTATCTCAGGATTTAATAATAATGTTTCAGGGCCAAATTTATGATAATTAATAACT 1083
Qy 181 GAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATATAAAACGTTGATTTGGT 240
Db 1084 GAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATATAAAACGTTGATTTGGT 1143
Qy 241 GTAGAAATTTACCAATCTCTGTTATTTATGTAAGATGCAAAAGAGTGTGATCTAC 300
Db 1144 GTAGAAATTTACCAATCTCTGTTATTTATGTAAGATGCAAAAGAGTGTGATCTAC 1203
Qy 301 GGAGGGGTAAACAATCATGAGGGAATCAATTTAGAAATTTCTTAAAGATAGTCTGTTAA 360
Db 1204 GGAGGGGTAAACAATCATGAGGGAATCAATTTAGAAATTTCTTAAAGATAGTCTGTTAA 1263
Qy 361 GTATCAATTCGATGGTATCCAAAGCCTATCTTTGATATTGAAAACAAATATAAAATGGTA 420
Db 1264 GTATCAATTCGATGGTATCCAAAGCCTATCTTTGATATTGAAAACAAATATAAAATGGTA 1323
Qy 421 ACTGCTCAAGAAATAGACTATAAAGTTAGAAAAATCTTTAAGATTAAGCAACTATAT 480
Db 1324 ACTGCTCAAGAAATAGACTATAAAGTTAGAAAAATCTTTAAGATTAAGCAACTATAT 1383
Qy 481 ACTAATGACCTCTTAATATCAACTGGATATATTAAGTTTCACTACCTAAGAAATAAGAA 540
Db 1384 ACTAATGACCTCTTAATATCAACTGGATATATTAAGTTTCACTACCTAAGAAATAAGAA 1443
Qy 541 AGTTTGGTTGATTTTCCCTGAACCAAGATTTTACTCAATCTTAAATATCTTATGATA 600
|||

Applicant
this is
Applicant

Applicant
this is
Applicant

Db 1324 ACTGCTCAAGATTAGACTATATAAAGTTGAGAAAATATCTTACAGATAATAAGCAACTATAT 1383
QY 481 ACTAATGACCTTCTAATATATGAAAGCTGGATATATAAAGTTTCATACCTTAAGAAATAAGAA 540
Db 1384 ACTAATGACCTTCTAATATATGAAAGCTGGATATATAAAGTTTCATACCTTAAGAAATAAGAA 1443
QY 541 AGTTTTTGTTGATTTTTCCTGAAACAGAAATTTACTCAATCTAAATATCTTATGATA 600
Db 1444 AGTTTTTGTTGATTTTTCCTGAAACAGAAATTTACTCAATCTAAATATCTTATGATA 1503
QY 601 TATAAGATAATGAACGCTTGACTCAAAACAAGCCAAATTTGAAGTCTTACCTAACACC 660
Db 1504 TATAAGATAATGAACGCTTGACTCAAAACAAGCCAAATTTGAAGTCTTACCTAACACC 1563
QY 661 AAG 663
Db 1564 AAG 1566

RESULT 5

US-08-882-431-15
; Sequence 15, Application US/08882431
; Publication No. US200309015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1837
; TYPE: Nucleic Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: DNA
US-08-882-431-15

Query Match 99.3%; Score 658.2; DB 8; Length 1837;
Best Local Similarity 99.5%; Pred. No. 2e-116;
Matches 660; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACAGACCCCGATCCAGCCAACTTCACAGATCTAGTTTGTAAACCTTCAAAAT 60
Db 904 CAACAGACCCCGATCCAGCCAACTTCACAGATCTAGTTTGTAAACCTTCAAAAT 963

QY 61 ATATATTTTCTTTATGAGGCTGACCTGTACTACAGAAATGTGAAATCTGTGATCAA 120
Db 964 ATATATTTTCTTTATGAGGCTGACCTGTACTACAGAAATGTGAAATCTGTGATCAA 1023
QY 121 CTTTATCTCACCATTATATATATATGTTTCAGGGCCAAATATGATAAATAAACT 180
Db 1024 CTTAGATCTCAGATTATATATATGTTTCAGGGCCAAATATGATAAATAAACT 1083
QY 181 GNACTTAAGACCAAGATGCGCACTTTATTTAAGGATAAAAGCTTTGATATTTATGCT 240
Db 1084 GAACTTAAAGAACCAAGATGCGCACTTTATTTAAGGATAAAAGCTTTGATATTTATGCT 1143
QY 241 GTAGAATATTACCATCTCTGTTTATTTATGTAAGGAGGAGTGCATGTATCTAC 300
Db 1144 GTAGAATATTACCATCTCTGTTTATTTAAGGAGGAGTGCATGTATCTAC 1203
QY 301 GGAGGGTAAACAAATCATGAGGGAATCATTTAGAAATTCCTTAAAGATAGTCGTTAA 360
Db 1204 GGAGGGTAAACAAATCATGAGGGAATCATTTAGAAATTCCTTAAAGATAGTCGTTAA 1263
QY 361 GTATCAATCGATGTTATCCAAAGCCCTATCTTTGATATTTGAACAAATAAAATGTTA 420
Db 1264 GTATCAATCGATGTTATCCAAAGCCCTATCTTTGATATTTGAACAAATAAAATGTTA 1323
QY 421 ACTGCTCAAGAAATAGACTATAAAGTTAGAAATATCTTACAGATAATAAGCAACTATAT 480
Db 1324 ACTGCTCAAGAAATAGACTATAAAGTTAGAAATATCTTACAGATAATAAGCAACTATAT 1383
QY 481 ACTAATGACCTTCTAATATATGAAAGCTGGATATATAAGTTTCATACCTTAAGAAATAAGAA 540
Db 1384 ACTAATGACCTTCTAATATATGAAAGCTGGATATATAAGTTTCATACCTTAAGAAATAAGAA 1443
QY 541 AGTTTTTGTTGATTTTTCCTGAAACAGAAATTTACTCAATCTAAATATCTTATGATA 600
Db 1444 AGTTTTTGTTGATTTTTCCTGAAACAGAAATTTACTCAATCTAAATATCTTATGATA 1503
QY 601 TATAAGATAATGAACGCTTGACTCAAAACAAGCCAAATTTGAAGTCTTACCTAACACC 660
Db 1504 TATAAGATAATGAACGCTTGACTCAAAACAAGCCAAATTTGAAGTCTTACCTAACACC 1563
QY 661 AAG 663
Db 1564 AAG 1566

RESULT 6

US-10-002-784A-15
; Sequence 15, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 15
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
US-10-002-784A-15

Query Match 99.0%; Score 656.6; DB 15; Length 1837;
Best Local Similarity 99.4%; Pred. No. 4.1e-116;
Matches 659; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACAGACCCCGATCCAGCCAACTTCACAGATCTAGTTTGTAAACCTTCAAAAT 60

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Db 904 CAACAGACCCGATCCAGCACTTCACAGATCTAGTTTGTATTAACCTTCAAAAT 963
Qy 61 ATATATTTCTTTATGAGGGTGACCCCTGTTACTCACGAGAAATGTGAATCTGTTGATCAA 120
Db 964 ATATATTTCTTTATGAGGGTGACCCCTGTTACTCACGAGAAATGTGAATCTGTTGATCAA 1023
Qy 121 CTTTATCTCACCATTAAATATATAATGTTTTCAGGGCCAAATTTATGATAAATTAATAACT 180
Db 1024 CTTAGATCTCAGGATTTAAATATATAATGTTTTCAGGGCCAAATTTATGATAAATTAATAACT 1083
Qy 181 GAACTTAAGAACCAAGAGATGCGCACTTTATTTAAGGATTAATAAAGCTTTGATATTTATGGT 240
Db 1084 GAACTTAAGAACCAAGAGATGCGCACTTTATTTAAGGATTAATAAAGCTTTGATATTTATGGT 1143
Qy 241 GTAGAATATTACCACTCTCTGTTATTTATGTGAATAATGCAGAAAGGAGTGCATGATCTAC 300
Db 1144 GTAGAATATTACCACTCTCTGTTATTTATGTGAATAATGCAGAAAGGAGTGCATGATCTAC 1203
Qy 301 GGAGGGGTAAACAATCATGAGGGCAATCACTTAGAATTTCTTAAAGATAGTCTGTAAA 360
Db 1204 GGAGGGGTAAACAATCATGAGGGCAATCACTTAGAATTTCTTAAAGATAGTCTGTAAA 1263
Qy 361 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATTAATAAATTAAGTA 420
Db 1264 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATTAATAAATTAAGTA 1323
Qy 421 ACTGCTCAAGAAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATTAAGCAACTATAT 480
Db 1324 ACTGCTCAAGAAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATTAAGCAACTATAT 1383
Qy 481 ACTAATGACCTTCTAAATGAACTGGATATATAAAGTTCTAATCTAATATCTTATGATA 540
Db 1384 ACTAATGACCTTCTAAATGAACTGGATATATAAAGTTCTAATCTAATATCTTATGATA 1443
Qy 541 AGTTTTCGTTGATTTTTCCTGAACCAAGATTTACTCAATCTAATATCTTATGATA 600
Db 1444 AGTTTTCGTTGATTTTTCCTGAACCAAGATTTACTCAATCTAATATCTTATGATA 1503
Qy 601 TATAAGATAATGAACGCTTGACTCAAAACCAAGCCAAATTTGAAGTCTACCTAACCAACC 660
Db 1504 TATAAGATAATGAACGCTTGACTCAAAACCAAGCCAAATTTGAAGTCTACCTAACCAACC 1563
Qy 661 AAG 663
Db 1564 AAG 1566
```

RESULT 7

US-10-002-784A-23

; Sequence 23, Application US/10002784A

; Publication No. US2003003664A1

; GENERAL INFORMATION:

/33

; APPLICANT: Ulrich, Robert G.

; TITLE OF INVENTION: Bacterial Superantigen Vaccines

; FILE REFERENCE: 003/233/SAP

; CURRENT APPLICATION NUMBER: US/10/002,784A

; CURRENT FILING DATE: 2001-11-26

; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776

; PRIOR FILING DATE: 97-06-25; 98-09-01

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: Apple Macintosh Microsoft Word 6.0

; SEQ ID NO 23

; LENGTH: 1419

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: mutant SpeA/mutant SpeB fusion

US-10-002-784A-23

Query Match

Best Local Similarity 98.3%; Score 651.8; DB 15; Length 1419;

Pred. No. 3.1e-115;

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Matches 656; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CAACAGACCCGATCCAGCACTTCACAGATCTAGTTTGTATTAACCTTCAAAAT 60
Db 4 CAACAGACCCGATCCAGCACTTCACAGATCTAGTTTGTATTAACCTTCAAAAT 63
Qy 61 ATATATTTCTTTATGAGGGTGACCCCTGTTACTCACGAGAAATGTGAATCTGTTGATCAA 120
Db 64 ATATATTTCTTTATGAGGGTGACCCCTGTTACTCACGAGAAATGTGAATCTGTTGATCAA 123
Qy 121 CTTTATCTCACCATTAAATATATAATGTTTTCAGGGCCAAATTTATGATAAATTAATAACT 180
Db 124 CTTGATCTCAGGATTTAAATATATAATGTTTTCAGGGCCAAATTTATGATAAATTAATAACT 183
Qy 181 GAACTTAAGAACCAAGAGATGCGCACTTTATTTAAGGATTAATAAAGCTTTGATATTTATGGT 240
Db 184 GAACTTAAGAACCAAGAGATGCGCACTTTATTTAAGGATTAATAAAGCTTTGATATTTATGGT 243
Qy 241 GTAGAATATTACCACTCTCTGTTATTTATGTGAATAATGCAGAAAGGAGTGCATGATCTAC 300
Db 244 GTAGAATATTACCACTCTCTGTTATTTATGTGAATAATGCAGAAAGGAGTGCATGATCTAC 303
Qy 301 GGAGGGGTAAACAATCATGAGGGCAATCACTTAGAATTTCTTAAAGATAGTCTGTAAA 360
Db 304 GGAGGGGTAAACAATCATGAGGGCAATCACTTAGAATTTCTTAAAGATAGTCTGTAAA 363
Qy 361 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATTAATAAATTAAGTA 420
Db 364 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATTAATAAATTAAGTA 423
Qy 421 ACTGCTCAAGAAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATTAAGCAACTATAT 480
Db 424 ACTGCTCAAGAAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATTAAGCAACTATAT 483
Qy 481 ACTAATGACCTTCTAAATGAACTGGATATATAAAGTTCTAATCTAATATCTTATGATA 540
Db 484 ACTAATGACCTTCTAAATGAACTGGATATATAAAGTTCTAATCTAATATCTTATGATA 543
Qy 541 AGTTTTCGTTGATTTTTCCTGAACCAAGATTTACTCAATCTAATATCTTATGATA 600
Db 544 AGTTTTCGTTGATTTTTCCTGAACCAAGATTTACTCAATCTAATATCTTATGATA 603
Qy 601 TATAAGATAATGAACGCTTGACTCAAAACCAAGCCAAATTTGAAGTCTACCTAACCAACC 660
Db 604 TATAAGATAATGAACGCTTGACTCAAAACCAAGCCAAATTTGAAGTCTACCTAACCAACC 663
Qy 661 AAG 663
Db 664 AAG 666
```

RESULT 8

US-09-870-759-19

; Sequence 19, Application US/09870759

; Patent No. US20020177551A1

; GENERAL INFORMATION:

; APPLICANT: TERMAN, David S

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

; FILE REFERENCE: 870759

; CURRENT APPLICATION NUMBER: US/09/870,759

; CURRENT FILING DATE: 2002-01-14

; PRIOR APPLICATION NUMBER: US 60/208,128

; PRIOR FILING DATE: 2000-05-30

; NUMBER OF SEQ ID NOS: 166

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 19

; LENGTH: 1031

; TYPE: DNA

; ORGANISM: Streptococcus pyogenes

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (79)..(831)

; OTHER INFORMATION:

US-09-870-759-19

Query Match 87.9%; Score 582.6; DB 9; Length 1031;
Best Local Similarity 97.1%; Pred. No. 5e-102;
Matches 636; Conservative 0; Mismatches 14; Indels 5; Gaps 4;

QY 10 CCCGATCCAAAGCCAACTTCACAGATCTAGTTTAGTTTAAACCTTCAAAATATATATTTT 69
DB 178 CCCAAGCCAGCCAAATTCACAGATCTAATTTAGTT-AAAACCTTCAAAATATATATTTT 236
QY 70 CTTTATGAGGGTGACCCCT-GTTACTCACGAGAAATGTGAATCTGTGTGATCAACTTTTATC 128
DB 237 CTTTATGAGGGTGACCCCTGTTACTCACGAGAAATGTGAATCTGTGTGATCAACTTTTATC 296
QY 129 TCACCAATTTAAATATAATGTTTCAGGGCCAAATATATGATAATTAATAAAGTGAACCTTAA 188
DB 297 ACACGATTTAAATATAATGTTTCAGGGCCAAATATATGATAATTAATAAAGTGAACCTTAA 356
QY 189 GAACCAAGAGATGGCAACTTTTAAAGGATAAAACGTTTGATATTTATGGTGTAGAAATA 248
DB 357 GAACCAAGAGATGGCAACTTTTAAAGGATAAAACGTTTGATATTTATGGTGTAGAAATA 416
QY 249 TTACCATCTCTGTTTATTTATGTAATAATCGAAGAGAGTGCATGATCTACGGAGGGGT 308
DB 417 TTACCATCTCTGTTTATTTATGTAATAATCGAAGAGAGTGCATGATCTCTACGGAGGGGT 476
QY 309 AACCAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAAGTATCAAT 368
DB 477 AACCAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAAGTATCAAT 536
QY 369 CGATGGTATCCAAAGCCCTATCATTTGATATGAAACAAATAAAATGTTAACTGCTCA 428
DB 537 CGATGGTATCCAAAGCCCTATCATTTGATATGAA--CAAATAAAATGTTAACTGCTCA 594
QY 429 AGAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATAAGCAACTATATTAATGG 488
DB 595 AGAATTAG-CTATACAGTTAGAAAATATCTTACAGATAATAAGCAACTATATTAATGG 653
QY 489 ACCTTCTAAATATGAACCTGGATATATAAAGTTCTACCTAAGATAAAGAAAGTTTGG 548
DB 654 ACCTTCTAAATATGAACCTGGATATATAAAGTTCTACCTAAGATAAAGAAAGTTTGG 713
QY 549 GTTTCATTTTCCCTGACCAAGAAATTTACTCAATCTAAATCTTATGATATAAAGA 608
DB 714 GTTTCATTTTCCCTGACCAAGAAATTTACTCAATCTAAATCTTATGATATAAAGA 773
QY 609 TAATGAACCGTTGATCTCAACACAGCCAAATTTGAAGTCTACCTAACCAACCAAG 663
DB 774 TAATGAACCGTTGATCTCAACACAGCCAAATTTGAAGTCTACCTAACCAACCAAG 828

RESULT 9

US-09-751-708A-19
; Sequence 19, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1031
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(831)
; OTHER INFORMATION:

US-09-751-708A-19

Query Match 87.9%; Score 582.6; DB 10; Length 1031;
Best Local Similarity 97.1%; Pred. No. 5e-102;
Matches 636; Conservative 0; Mismatches 14; Indels 5; Gaps 4;

QY 10 CCCGATCCAAAGCCAACTTCACAGATCTAGTTTAGTTTAAACCTTCAAAATATATATTTT 69
DB 178 CCCAAGCCAGCCAAATTCACAGATCTAATTTAGTT-AAAACCTTCAAAATATATATTTT 236
QY 70 CTTTATGAGGGTGACCCCT-GTTACTCACGAGAAATGTGAATCTGTGTGATCAACTTTTATC 128
DB 237 CTTTATGAGGGTGACCCCTGTTACTCACGAGAAATGTGAATCTGTGTGATCAACTTTTATC 296
QY 129 TCACCAATTTAAATATAATGTTTCAGGGCCAAATATATGATAATTAATAAAGTGAACCTTAA 188
DB 297 ACACGATTTAAATATAATGTTTCAGGGCCAAATATATGATAATTAATAAAGTGAACCTTAA 356
QY 189 GAACCAAGAGATGGCAACTTTTAAAGGATAAAACGTTTGATATTTATGGTGTAGAAATA 248
DB 357 GAACCAAGAGATGGCAACTTTTAAAGGATAAAACGTTTGATATTTATGGTGTAGAAATA 416
QY 249 TTACCATCTCTGTTTATTTATGTAATAATCGAAGAGAGTGCATGATCTACGGAGGGGT 308
DB 417 TTACCATCTCTGTTTATTTATGTAATAATCGAAGAGAGTGCATGATCTCTACGGAGGGGT 476
QY 309 AACCAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAAGTATCAAT 368
DB 477 AACCAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAAGTATCAAT 536
QY 369 CGATGGTATCCAAAGCCCTATCATTTGATATGAAACAAATAAAATGTTAACTGCTCA 428
DB 537 CGATGGTATCCAAAGCCCTATCATTTGATATGAA--CAAATAAAATGTTAACTGCTCA 594
QY 429 AGAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATAAGCAACTATATTAATGG 488
DB 595 AGAATTAG-CTATACAGTTAGAAAATATCTTACAGATAATAAGCAACTATATTAATGG 653
QY 489 ACCTTCTAAATATGAACCTGGATATATAAAGTTCTACCTAAGATAAAGAAAGTTTGG 548
DB 654 ACCTTCTAAATATGAACCTGGATATATAAAGTTCTACCTAAGATAAAGAAAGTTTGG 713
QY 549 GTTTCATTTTCCCTGACCAAGAAATTTACTCAATCTAAATCTTATGATATAAAGA 608
DB 714 GTTTCATTTTCCCTGACCAAGAAATTTACTCAATCTAAATCTTATGATATAAAGA 773
QY 609 TAATGAACCGTTGATCTCAACACAGCCAAATTTGAAGTCTACCTAACCAACCAAG 663
DB 774 TAATGAACCGTTGATCTCAACACAGCCAAATTTGAAGTCTACCTAACCAACCAAG 828

RESULT 10

US-09-870-759-11
; Sequence 11, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (118)..(918)
; OTHER INFORMATION:

US-09-870-759-11

Query Match 25.2%; Score 167.4; DB 9; Length 1095;
Best Local Similarity 59.0%; Pred. No. 1.7e-22;
Matches 382; Conservative 0; Mismatches 226; Indels 39; Gaps 4;

QY 56 AAAAAATATATTTCTTTATGAGGGTGACCCCTGTTACTCAGGAGAAATGTGAAATCTCTTG 115
DB 263 AAAAAATGAAAGTTTTATATGATGATCATTTATGATCAGCAACTAAAGTTAAAGTCTGTAG 322

QY 116 ATCAACTTTTATCTCACCAATTTAATATATATATGTTTCAGG-----GCCAAATATG 166
DB 323 ATAAATTTTGGCACATGATTTAATTTATACATTAGTGATAAAAAAAGTGAATAATATG 382

QY 167 ATAAATTAAGAACTTAAGAAACCAAGAGATGGCAACTTTATTTAAGGATTAAGAAACG 226
DB 383 ACAAAGTGAAGAAACAGAGTTTATTAATGAAGTTTATAGCAAGAAAGTACAAAGATGAAGTAG 442

QY 227 TTGATATTTATGTTGTAGATATTTACCATCTCTGTTATTTAT----- 268
DB 443 TTGATGTTATGATCAAAATTTACTATGTAACCTGCTATTTTTCATCCAAAGATTAATGTAG 502

QY 269 GTGAAAATGCAGAAAGAGTGATCTACGGAGGGGTAAACAAATCATGAAGGGAATC 328
DB 503 GTAAAGTTACAGGTGGCAAACTTTGTATGTATGAGGGAATACAAACATGAAGGAAACC 562

QY 329 ATTTAGAAATTCCTA-----AAAAGATAGTCGTTTAAAGTATCAATCGATGGTATCCAAA 382
DB 563 ACTTTGATAATGGGAACCTTACAAAATGTACTTTAAGAGTTTATGAAAATTAAGAAACA 622

QY 383 GCCTATCATTTGATTTGAAACAAATTAAGAAATGTTAACTGCTCAAGAAATTAAGACTATA 442
DB 623 CAATTTCTTTTGAAGTGCAAACTGATGAAGAAAGTGAACAGCTCAAGAACTAGACATAA 682

QY 443 AAGTTAGAAATATCTTTACAGATAATAAGCAACTATATCTAATAGGACCTTCTAAATATG 502
DB 683 AAGCTAGAAATTTTAAATTAATAAAAAATTTGTATGAGTTTAAACAGTTTACCATATG 742

QY 503 AAACCTGATATATAAGTTCTACCTAAGAAATAAGAAAGTTTGTGTTGTTGATTTTTC 562
DB 743 AAACAGGATATATAAATTTATTGAAAATAACGGCAATACCTTTTGGTATGATATGATGC 802

QY 563 CTGAACACAG-----AATTTACTCAATCTAAATCTTATGATATATAAGATATGAAA 616
DB 803 CTGACACAGGCGAATAGTTGACCAATCTAAATTTAATGATGTACACGACATATAA 862

QY 617 CGTTTGACTCAACACAGCAAAATTTGAAGTCTACCTAACCAACCAAG 663
DB 863 CGGTTGATTTCTAAAGTGTGAAGATAGAGTCCACCTTACAAACAAG 909

RESULT 11

US-09-751-708A-11
; Sequence 11, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (118)..(918)
; OTHER INFORMATION:

US-09-751-708A-11

Query Match 25.2%; Score 167.4; DB 10; Length 1095;
Best Local Similarity 59.0%; Pred. No. 1.7e-22;
Matches 382; Conservative 0; Mismatches 226; Indels 39; Gaps 4;

QY 56 AAAAAATATATTTCTTTATGAGGGTGACCCCTGTTACTCAGGAGAAATGTGAAATCTCTTG 115
DB 263 AAAAAATGAAAGTTTTATATGATGATCATTTATGATCAGCAACTAAAGTTAAAGTCTGTAG 322

QY 116 ATCAACTTTTATCTCACCAATTTAATATATATATGTTTCAGG-----GCCAAATATG 166
DB 323 ATAAATTTTGGCACATGATTTAATTTATACATTAGTGATAAAAAAAGTGAATAATATG 382

QY 167 ATAAATTAAGAACTTAAGAAACCAAGAGATGGCAACTTTATTTAAGGATTAAGAAACG 226
DB 383 ACAAAGTGAAGAAACAGAGTTTATTAATGAAGTTTATAGCAAGAAAGTACAAAGATGAAGTAG 442

QY 227 TTGATATTTATGTTGTAGATATTTACCATCTCTGTTATTTAT----- 268
DB 443 TTGATGTTATGATCAAAATTTACTATGTAACCTGCTATTTTTCATCCAAAGATTAATGTAG 502

QY 269 GTGAAAATGCAGAAAGAGTGATCTACGGAGGGGTAAACAAATCATGAAGGGAATC 328
DB 503 GTAAAGTTACAGGTGGCAAACTTTGTATGTATGAGGGAATACAAACATGAAGGAAACC 562

QY 329 ATTTAGAAATTCCTA-----AAAAGATAGTCGTTTAAAGTATCAATCGATGGTATCCAAA 382
DB 563 ACTTTGATAATGGGAACCTTACAAAATGTACTTTAAGAGTTTATGAAAATTAAGAAACA 622

QY 383 GCCTATCATTTGATTTGAAACAAATTAAGAAATGTTAACTGCTCAAGAAATTAAGACTATA 442
DB 623 CAATTTCTTTTGAAGTGCAAACTGATGAAGAAAGTGAACAGCTCAAGAACTAGACATAA 682

QY 443 AAGTTAGAAATATCTTTACAGATAATAAGCAACTATATCTAATAGGACCTTCTAAATATG 502
DB 683 AAGCTAGAAATTTTAAATTAATAAAAAATTTGTATGAGTTTAAACAGTTTACCATATG 742

QY 503 AAACCTGATATATAAGTTCTACCTAAGAAATAAGAAAGTTTGTGTTGTTGATTTTTC 562
DB 743 AAACAGGATATATAAATTTATTGAAAATAACGGCAATACCTTTTGGTATGATATGATGC 802

QY 563 CTGAACACAG-----AATTTACTCAATCTAAATCTTATGATATATAAGATATGAAA 616
DB 803 CTGACACAGGCGAATAGTTGACCAATCTAAATTTAATGATGTACACGACATATAA 862

QY 617 CGTTTGACTCAACACAGCAAAATTTGAAGTCTACCTAACCAACCAAG 663
DB 863 CGGTTGATTTCTAAAGTGTGAAGATAGAGTCCACCTTACAAACAAG 909

RESULT 12

US-10-354-948-1
; Sequence 1, Application US/10354948
; Publication No. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; Elmslie, Robyn E.
; Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25


```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/354,948
FILING DATE: 29-Jan-2003
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 773 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: CDS
LOCATION: 1..768
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-354-948-1

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Query Match	25.2%	Score 166.8	DB 13	Length 773
Best Local Similarity	59.1%	Pred. No. 1.9e-22		
Matches 384	Conservative 0	Mismatches 221	Indels 45	Gaps 4
QY	56	AAATATATATTTTCTTTATGAGGGTGACCTGTTACTCAGAGAAATGTGAAATCTGTG	115	
Db	113	AAAATATGAAAGTTTGTATGATGATAATCATGTATCAGCAATAAATGCTTAAATCTATAG	172	
QY	116	ATCAACTTTTATCTCACCAATTTAATATATATTAATGTTTCAGGCGCA-----AATATG	166	
Db	173	ATCAATTTCTATACCTTGACTTATATATCTTATTAAGGACACTAAGTTAGGGAATATG	232	
QY	167	ATAAATTAATAAATCTGAACCTTAAGAACCAAGAGATGGCAACTTTTATTTAAGGATAAAAAACG	226	
Db	233	ATAATGTTCCAGTCCGAATTTAAAAACAAGATTTAGCTGATAAATACAAAGATAAATACG	292	
QY	227	TTGATATTTTATGGTGATGATAATTTACCATCTCTGTTATTTTATGTGAAAA-----	275	
Db	293	TAGATGGTTTGGAGCTAAATTTATTTATTTATCAATGTTATTTTCTTAAAAAAACGAATGATA	352	
QY	276	-----TGCAGAAAGGAGTGCATGTATCTACGGAGGGGTAAACAAATCATG	319	
Db	353	TTAATTCGCATCAAACTGACAAACGAAAAACTTGTATGTATGGTGGTAACTGAGGATA	412	
QY	320	AAGGGAATCAATTAGAAAAATTCCTAAAAGATAGTCGTTAAAGTATCAATCGATGGTATCC	379	
Db	413	ATGGAACCAAATTAGATAAAATATAGAAGTATTACTGTTCCGGTATTTGAAGATGGTAAAA	472	
QY	380	AAAGCCTATCATTTGATATGAAACAATAAABAAATGTAATCTGCTCAGAATTAGACT	439	
Db	473	ATTATTATCTTTTGACGTACAACACTAATAGAAAAAGGTGACTGCTCAGAATTTAGATT	532	
QY	440	ATAAAGTTGAAAAATATCTTACAGATAATAAGCAACTATATCTAATATGGACCTTCTAAAT	499	
Db	533	ACCTAATCTGCTCATTTTGGTGAATAATAAAAACTATATGATTTAAACAATCGCCCTT	592	
QY	500	ATGAACCTGGATATATAAAGTTCATACCTAAGAAATAAAGAAAGTTTTTGGTTGATTTTT	559	
Db	593	ATGAACGGGATATATTTAAATTTTATA---GAAAAATGAGAATAGCTTTTGGTATGACATGA	649	
QY	560	TCCTCTGAACCAAG-----AATTTTACTCAATCTCAAAATCTTTATGATATATAAGAGATAATG	613	
Db	650	TGCTCTGACCAACGAGATAAATTTGACCAATCTAAATATTTAATGATGTCACATGACATA	709	
QY	614	AAACGGTTGACTCAACACAAAGCAAATTTGAAGTCTTACTTAACAACAAG	663	

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Db      710  AAATGGTTGATCTTAAAGATGTGAAGATTGAAGTTTATCTTACGACAAAG 759

RESULT 13
US-09-870-759-1
; Sequence 1, Application US/09870759
; Patent No. US2020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEO
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Staphylococcus sp.
US-09-870-759-1

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Query Match	25.2%;	Score 166.8;	DB 9;	Length 801;
Best Local Similarity	59.1%;	Pred. No. 2e-22;		
Matches 384;	Conservative 0;	Mismatches 221;	Indels 45;	Gaps 4
QY	56	AAAATATATATTTCTTTATGAGGGTGACCTGTTACTACGAGAAATGTGAAATCTGTG	115	
Db	146	AAAATATGAAGTTTGTATGATGATTAATCATGTATCAGCATATAACGTTAAATCTATAG	205	
QY	116	ATCAACTTTTATCTCACCAATTAATATPATTAATGTTTCAGGCGCA-----AATTATG	166	
Db	206	ATCAATTTTCATACTTTGACTTAATAATATCTATTAAAGGACATAAGTTAGGGAAATTATG	265	
QY	167	ATAAATTTAAAACTGAACTTTAAGAACCAAGAGATGGCAACTTTATTTAAAGATATAAACG	226	
Db	266	ATAAATGTTGAGTCGAATTTTAAACAACAAAGATTTAGCTGATAATACAAAGATAAATACG	325	
QY	227	TTGATATTTATGGTGTAGAAATTTACCATCTCTGTTATTTATGTGAAAA-----	275	
Db	326	TAGATGTTTGGAGCTAATTAATTATCAATGTTATTTTCTTAAAAAACGAATGATA	385	
QY	276	-----TGCAAGAAAGGTGCATGTATCTACGAGGGGTAACAATCATG	319	
Db	386	TTAAATTGCGATCAAACTGACAAACGAAAACTTGATGTATGGTGGTGAACGTGAGATA	445	
QY	320	AAGGGAAATCAATTTAGAAAATTCCTTAAAAAGATAGTCGTTAAAGTATCAATCGATGGTATCC	379	
Db	446	ATGAAAACCAATTAGATAAATAATAGAAGTATTACTGTTTCGGGTATTTGAGAGTGTAAAA	505	
QY	380	AAAGCCTATCATTTGATATTGAAACAAATATAAAAAATGGTAACTGCTCAAGAAATTAGACT	439	
Db	506	ATTTATTATCTTTTGGACTACAAACTAATAAGAAAAAGGTGACTGCTCAAGAANTAGATT	565	
QY	440	ATAAGCTGAAAAATATCTTACAGATAATAAGCAACTATATCTAATGGACCTTCTAAAT	499	
Db	566	ACCTAACTCGTCACATTTTGGTCAAAAATATAAAAACTTAATGAATTTAAACAATCGCCTT	625	
QY	500	ATGAAACTGATATATAAAGTTTCATCTTAAGAAATAAAGAAAGATTTTGTGTTGAATTTT	559	
Db	626	ATGAAACGGGATATATTAATTTTATA--GAAATGAGATAGCTTTTGGTATGACATGA	682	
QY	560	TCCTCTGAACGAG-----AATTTTACTCTAAATATCTTATGATATAAAGATAATG	613	
Db	683	TGCTGACACGAGAGATAAATTTGACCAATCTAAATATTTTAATGATGTCATGACATA	742	
QY	614	AAACGCTTGACTCAAAACAACAGCCAAATTTGAAGTCTACCTTAAACAAACGAG	663	
Db	743	AAATGTTGATCTTAAAGATGTGAAGATTGAAGTTTATCTTACGACAAAAA792		

RESULT 14

US-09-751-708A-1
; Sequence 1, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Staphylococcus sp.
US-09-751-708A-1

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Query Match      25.2%; Score 166.8; DB 10; Length 801;
Best Local Similarity 59.1%; Pred. No. 2e-22; Indels 45; Gaps 4;
Matches 384; Conservative 0; Mismatches 221;

QY 56 AAAATATATATATTTCTTTATGAGGGTGACCCCTGTTACTCAGAGAAATGTGAAATCTGTG 115
Db 146 AAAATATGAAAGTTTGTATGATGATAATCAATGATCAGCAATAAACGTTAAATCTATAG 205

QY 116 ATCAACTTTTATCTCACCATTATATATATATATATATATATATATATATATATATAT 166
Db 206 ATCAATTTCTTACTTTGACTTAATATATATCTTATTAAGGACACTAAGTTAGGGAATTATG 265

QY 167 ATAAATTAATAAAGTCAACTTAAGAACCAAGAGATGCGCAACTTTATTAAGGATAAAACG 226
Db 266 ATATGTTTCGAGTCGAATTTTAAACCAAGATTTAGCTGATAAATACAAAGATAAATACG 325

QY 227 TTGATATTTATGTTGATAGATATATACCATCTCTGTTATTTATGTAATAA----- 275
Db 326 TAGATGTTGTTGGAGCTAATTTATTTATCAATGTTATTTTCTAAACCAAGATGATA 385

QY 276 -----TGCAGAAAGGAGTGATGATCTACGAGGAGGTTAAGGAGGTTAAGGAGGTTAAG 319
Db 386 TTAATTCGCATCAAACTGACAAACGAAACCTTGTATGTTGTTGTTGTTGTTGTTGTTGTTG 445

QY 320 AAGGAATCAITTTAGAAATTCCTAAAGAGATAGTCTGTTAAAGTATCAATCGATGTTATCC 379
Db 446 ATGNAACCAATTAGATTAATATAGAGATTTACTGTTTCGGGTATTTGGAAGTGTAAAA 505

QY 380 AAAGCCTATCATTTGATATGAAACAAATAAATAAATAAATAAATAAATAAATAAATAAATA 439
Db 506 ATTTATTTATCTTTTGACGTACAACTAATAAGAAAGGTTGACTGCTCAAGAAATTAGATT 565

QY 440 ATAAAGTTAGAAATATCTTACAGTATATAGCAACTATATATATATATATATATATATATAT 499
Db 566 ACCTAATCTGTCATTTTGTGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 625

QY 500 ATGAACTGGATATATAAAGTTTCATCTAAGAAATAAAGAAAGTTTGTGTTGTTGTTGTTT 559
Db 626 ATGAAACGGGATATATTAATTTATA-----GAAATGCAATAGCTTTTGGTATGACATGA 682

QY 560 TCCCTGAACCCAG-----AATTTACTCAATCTAAATATCTTATGATATATAAAGATATG 613
Db 683 TGCCTGCACCAAGGAGATAAATTTGACCAATCTAAATATTTAATGATGATACATGACATA 742

QY 614 AAAGCTTTGACTCAACACAGCCAAATTTGAAGTCTACCTAACCAACCAAG 663
Db 743 AAATGGTTGATCTTAAAGATGTGAGATTGAAGTTTATCTTACGACAAAG 792
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RESULT 15

US-09-870-759-2
; Sequence 2, Application US/09870759
; Patent No. US2002017551A1
; GENERAL INFORMATION:

; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 886
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-870-759-2

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Query Match      25.2%; Score 166.8; DB 9; Length 886;
Best Local Similarity 59.1%; Pred. No. 2e-22; Indels 45; Gaps 4;
Matches 384; Conservative 0; Mismatches 221;

QY 56 AAAATATATATATTTCTTTATGAGGGTGACCCCTGTTACTCAGAGAAATGTGAAATCTGTG 115
Db 188 AAAATATGAAAGTTTGTATGATGATAATCAATGATCAGCAATAAACGTTAAATCTATAG 247

QY 116 ATCAACTTTTATCTCACCATTATATATATATATATATATATATATATATATATATAT 166
Db 248 ATCAATTTCTTACTTTGACTTAATATATCTTATTAAGGACACTAAGTTAGGGAATTATG 307

QY 167 ATAAATTAATAAAGTCAACTTAAGAACCAAGAGATGCGCAACTTTATTAAGGATAAAACG 226
Db 308 ATATGTTTCGAGTCGAATTTTAAACCAAGATTTAGCTGATAAATACAAAGATAAATACG 367

QY 227 TTGATATTTATGTTGATAGATATATACCATCTCTGTTATTTATGTAATAA----- 275
Db 368 TAGATGTTGTTGGAGCTAATTTATTTATCAATGTTATTTTCTAAACCAAGATGATA 427

QY 276 -----TGCAGAAAGGAGTGATGATCTACGAGGAGGTTAAGGAGGTTAAGGAGGTTAAG 319
Db 428 TTAATTCGCATCAAACTGACAAACGAAACCTTGTATGTTGTTGTTGTTGTTGTTGTTGTTG 487

QY 320 AAGGAATCAITTTAGAAATTCCTAAAGAGATAGTCTGTTAAAGTATCAATCGATGTTATCC 379
Db 488 ATGNAACCAATTAGATTAATATAGAGATTTACTGTTTCGGGTATTTGGAAGTGTAAAA 547

QY 380 AAAGCCTATCATTTGATATGAAACAAATAAATAAATAAATAAATAAATAAATAAATAAATA 439
Db 548 ATTTATTTATCTTTTGACGTACAACTAATAAGAAAGGTTGACTGCTCAAGAAATTAGATT 607

QY 440 ATAAAGTTAGAAATATCTTACAGTATATAGCAACTATATATATATATATATATATATATAT 499
Db 608 ACCTAATCTGTCATTTTGTGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 667

QY 500 ATGAACTGGATATATAAAGTTTCATCTAAGAAATAAAGAAAGTTTGTGTTGTTGTTGTTT 559
Db 668 ATGAAACGGGATATATTAATTTATA-----GAAATGCAATAGCTTTTGGTATGACATGA 724

QY 560 TCCCTGAACCCAG-----AATTTACTCAATCTAAATATCTTATGATATATAAAGATATG 613
Db 725 TGCCTGCACCAAGGAGATAAATTTGACCAATCTAAATATTTAATGATGATACATGACATA 784

QY 614 AAAGCTTTGACTCAACACAGCCAAATTTGAAGTCTACCTAACCAACCAAG 663
Db 785 AAATGGTTGATCTTAAAGATGTGAGATTGAAGTTTATCTTACGACAAAG 834
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Job time : 426 secs

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